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SEQ ID NO 3
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Matches 1005;
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ALIGNMENTS

Sequence 3, Application Patent No. 6387676 APPLICANT: Virca, Duke
APPLICANT: Bird, Timothy A.
APPLICANT: Anderson, Dirk M.
APPLICANT: Marken, John S.
TITLE OF INVENTION: Human cDNAs Encoding Polypeptides Having
FILE REFERENCE: 2877-US
CURRENT APPLICATION NUMBER: US/09/509,902A
CURRENT FILING DATE: 1999-08-03
NUMBER OF SEQ ID NOS: 16 1 GCTCTGAGCCCCGGCGCGCCCCGGGCCCAACGAACGACGGGGCGAGATGCGAGCCACC CCCTGCCTGTTGCCCCTGAGCCCACCTACTGCTCCAGATCGTGCAACTGCTGTGGCCACT GCTCTGAGCCCCGGCGCCCCGGGCCCACGCGGAACGACGGGGCGAGATGCGAGCCACCC GCCCTGCACTGCCCTACAGGCACTGAGTATACCTGCAAGGTGTACCCCGTCCAGGAAGCC CCTCTGGCTGCTGCGGGTTCCCTGTCCAGGAAGAAGCGGTTGGAGTTGGATGACAAC CCTCTGGCTGCTCCTGCGGGTTCCCTGTCCAGGAAGAAGCGGTTGGAGTTGGATGACAAC CCTGCCTGTTGCCCCTGAGCCCACCTACTGCTCCAGATCGTGCAACTGCTGTGGCCACT 319 TTAGATACCGAGCGTCCCGTCCAGAAACGAGCTCGAAGTGGGCCCCAGCCCAGACTGCCC TTAGATACCGAGCGTCCCGTCCAGAAACGAGCTCGAAGTGGGCCCCAGCCCAGACTGCCC Conservative **eapiens** Ver. 48.8%; US/09509902A 2.0 0; Score 1004.4; DB 4; Pred. No. 4.8e-207; 0; Mismatches 1; 4 Length 1085; <u>..</u> Kinase Functions 439 379)300 120 259 180 199 139 60 0

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SOPTWARE: PastSI SEQ ID NO 135
LENGTH: 2559
LETYPE: DNA
ORGANISM: Homo 6
US-09-220-132-135
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Matches 566;
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                                                                                                                                                                                                                                                                                                                                                     Sequence 135, Application US/09220132 Patent No. 6506607
                                                                                                                                                                               APPLICANT: Shyjan, Andrew W.

TITLE OF INVENTION: METHODS AND COMPOSITONS/BOR THE IDENTIFICATION INTITLE OF INVENTION: OP PROSTATE CANCER THEMAPIES AND THE DIAGNOSIS (PILE REFERENCE: 07334-074001

FILE REFERENCE: 07334-074001

CURRENT APPLICATION NUMBER: US/09/220,132

CURRENT FILING DATE: 1998-12-23

PRIOR APPLICATION NUMBER: US 60/079,303

PRIOR PILING DATE: 1998-03-25

PRIOR PILING DATE: 1998-03-25

PRIOR PILING DATE: 1997-12-24

NUMBER: OF SEQ. ID NOS: 191
                                            Local Similarity 94.0
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US-08-146-421-4/c|

Sequence 4, Application US/08146421

Sequence 4, Application US/08146421

Patent No. 5543499

GENERAL INFORMATION:
APPLICANT: BREWER, GARY

TITLE OP INVENTION: ANTI-TUMOR PROPERTIES

NUMBER OP SEQUENCES: 9

CORRESPONDENCE ADDRESS:
ADDRESSE: DILMORTH & BARRESE

STREET 4430 LA JOLLA VILLAGE DRIVE, SUITE

CITY: SAN DIEGO

STATE: CALIFORNIA

COUNTRY: US.A.

ZIP: 92122

COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERAPTING SYSTEM: PC-DOS/MS-DOS
SOPTMARE: Patentin Release #1.0, Version #1

CURRENT APPLICATION NUMBER: US/08/146,421

PILMO DATE: 29-OCT-1993

CLASSIFICATION NUMBER: US/08/146,421

PILMO DATE: 29-OCT-1993

CLASSIFICATION NUMBER: 31,286

REGISTRATION NUMBER: 31,286

REGISTRATION: 1NFORMATION:
TELEPOME: 619-546-4410

TELEPOME: 619-546-4410

TELEPAX: 619-453-2839

INFORMATION GN. SEQ ID NO: 4:
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1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*

2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*

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US-10-084-817-300

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Sequence 9, Appli
Sequence 7, Appli
Sequence 271, Appli
Sequence 3, Appli
Sequence 560, App
Sequence 519, Appl
Sequence 116, Appl
Sequence 100, Appl
Sequence 269, Appl
Sequence 168, Appl
Sequence 168, Appli
Sequence 1, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 525, Appli
Sequence 492, Appli
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ALIGNMENTS

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TITLE OF INVENTION: No. U520020034780A1e1 H
TITLE OF INVENTION: Therefor
FILE REFERENCE: 3580/209996
CURRENT APPLICATION NUMBER: U5/09/799,875
CURRENT APPLICATION NUMBER: 60/182,059
PRIOR APPLICATION NUMBER: 60/182,059
PRIOR FILING DATE: 2000-02-11
PRIOR APPLICATION NUMBER: 09/659,287
PRIOR APPLICATION NUMBER: 09/659,287
PRIOR PILING DATE: 2000-09-12
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PASTSEQ for Windows Version 4.0
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APPLICANT: Meyers, Rachel
APPLICANT: Kapeller-Libermann, Rosana
APPLICANT: Williamson, Mark
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Best Local Similarity 99.8
Matches 1072; Conservative
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TYPE: DNA
ORGANISM: Homo sapiens
121 CCCAGACTGCCCCCCTGCCTGTTGCCCCTGAGCCCACCTACTGCTCCAGATCGTGCAACT 180
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                                                               TTGGATGACCAACTTAGATACCGAGCGTCCCGTCCAGAAACGAGCTCGAAGTGGGCCCCAG
                                                                                                                        ATGCGAGCCACCCCTCTGGCTGCTCCTGCGGGTTCCCAGGAAGAAGCGGTTGGAG
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                                                                                                                                                                                                       Score 1070.8; DB 9;
Pred. No. 3.7e-272;
0; Mismatches 2;
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RESULT 2
US-09-799-875-7
I Sequence 7, Application US/09799875
Patent No. US20020034780A1
GENERAL INFORMATION:
APPLICANT: Meyers, Rachel
APPLICANT: Welliamson, Mark
APPLICANT: Williamson, Mark
TITLE OF INVENTION: No. US20020034780A1el Human
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                                                                                                              CCCTTAGCCCCAACCCGATCCCATCTCTGGGAGGCTGCCCAGGTGGTCCCTGATGGACTG
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TYPE: DNA
ORGANISM: HOMO BAP1:
PEATURE:
NAME/KEY: CDS
LOCATION: (383)...(
US-09-799-875-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TITLE OF INVENTION: Therefor
; FILE REFERENCE: 35800/20996
; CURRENT APPLICATION NUMBER: US/09/799,875
; CURRENT FILING DATE: 2001-03-06
; PRIOR APPLICATION NUMBER: 60/182,059
; PRIOR APPLICATION NUMBER: 09/659,287
; PRIOR APPLICATION NUMBER: 09/659,287
; PRIOR FILING DATE: 2000-09-12
; NUMBER: OF SEQ ID NOS: 32
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 2389
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Similarity 99.8%;
72; Conservative
GCGTGCCCAGCCTACGTGGGACCTGAGATACTCAGCTCACGGGCCTCATACTCGGGCAAG
                                                  CGTGATCTCAAGCTGTGTCGCTTTGTCTTCGCTGACCGTGAGAGAAGAAGCTGGTGCTG
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Pred. No. 3.9e-272;
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1 ATGCGAGCCACCCCTCTGGCTGCTCCTGCGGGTTCCCTGTCCAGGAAGAAGCGGTTGGAG 60	Query Match 99.6%; Score 1069.2; DB 14; Length 2092; Best Local Similarity 99.7%; Pred. No. 1e-271; Matches 1071; Conservative 0; Mismatches 3; Indels 0; Gaps 0;	·	EQ ID NO 271 TELEVICITY EN CONTROL OF TYPE: DNA ORGANISM: Homo sapiens	PRIOR APPLICATION NUMBER: 09/488,725 PRIOR PILING DATE: 2000-01-21 NUMBER OF SEQ ID NOS: 331 SOFTWARE: DE FL GENES Version 1.0	; PRIOR APPLICATION NUMBER: 09/598,042 ; PRIOR FILING DATE: 2000-06-20 ; PRIOR PPLICATION NUMBER: 09/552,317 ; PRIOR FILING DATE: 2000-04-25		APPLICANT: Zhang, Jie APPLICANT: Qian, Xiaohong B. APPLICANT: Drmanac, Radoje T. TITLE OF INVENTION: No. US20020197679Alel Nucleic Acids and	APPLICANT: Chen, Rui-hong APPLICANT: Wang, Dunrui APPLICANT: Wang, Dinwei APPLICANT: Weng, Zhiwei APPLICANT: Weng, Tom	APPLICANT: Ma, Yunqing APPLICANT: Wang, Jian-Rui APPLICANT: Zhao, Qing A. APPLICANT: Ren, Feiyan	Liu, Che Asundi, Xu, Chon Zhou, Pi	ance 27	-271	1021 GGGCTGGACGAAGCCAGGAAAGAGAGAGACAGAGAGAGTTCTGTATGGC 1074 	961 CCCTTAGCCCCAACCCGATCCCATCTCTGGGAGGCTGCCCAGGTGGTCCCTGATGGACTG 1020	901 GCTGAACGGCTCACAGCCACAGGCATCCTCCTGCACCCCTGGCTGCGACAGGACCCGATG 960	841 CCTGCAGGCCTCTCGGCCCCTGCCCGCTGTCTGGTTCGCTGCCTCCT	781 TTCCAGGACTCGGAGCCTGTCCTGCTCTTCGGCAAGATCCGCCGCGGGGCCTACGCCTTG 840
RESULT 4 US-10-024-6 ; Sequence	g 43	Db Qy	Db	B &	g Qy	D Q	дь Q Y	B &	Db Qy	Db Qy	ОУ	D Qy	B &	gg dg	B &	? _. B	o p
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Publication No. US20030036051A1

GENERAL IMPORMATION:
APPLICANT: Virca, Duke
APPLICANT: Bird, Timothy A.
APPLICANT: Bird, Timothy A.
APPLICANT: Bard, Timothy A.
APPLICANT: Marken, John S.
TITLE OF INVENTION: Functions
ITITLE OF INVENTION: Functions
FILE REFERENCE: 2877-US
CURRENT APPLICATION NUMBER: US/10/024,828
CURRENT FILING DATE: 2001-12-18
PRIOR APPLICATION NUMBER: US/09/509,902A
PRIOR APPLICATION NUMBER: US/09/509,902A
PRIOR FILING DATE: 1999-08-03
NUMBER OF SEQ ID NOS: 16
SOPTWARE: Patentin Ver. 2.0
SEQ ID NO 3
LENGTH: 1085
TYPE: DNA
ORGANISM: Homo sapiens
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Best Local S
Matches 957
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bal Similarity 99.9%;
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               GCGTGCCCAGCCTACGTGGGACCTGAGATACTCAGCTCACGGGCCTCATACTCGGGCAAG
                                                                         GAGAACCTGGAGGACTCCTGCGTGCTGACTGGGCCAGATGATTCCCTGTGGGACAAGCAC
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 GCGTGCCCAGCCTACGTGGGACCTGAGATACTCAGCTCACGGGCCTCATACTCGGGCAAG
                                                        GAGAACCTGGAGGACTCCTGCGTGCTGACTGGCCAGATGATTCCCTGTGGGACAAGCAC
                                                                                                                 CGTGATCTCAAGCTGTGTCGCTTTGTCTTCGCTGACCGTGAGAGGAAGAAGCTGGTGCTG
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Pred. No. 4.7e-242;
D; Mismatches 1;
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CURRENT APPLICATION NUMBER: US/09/925,301
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05882
PRIOR APPLICATION NUMBER: PCT/US00/05882
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR PILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1694
SOPTWARE: Patentin Ver. 2.0
SEQ ID NO 260
LENGTH: 2048
TYPE: DNA
ORGANISM: Homo mapiens
PEATURE:
NAME/KEY: misc_feature
LOCATION: (66)
OTHER INFORMATION: n equals a,t,9, or c
NAME/KEY: misc_feature
LOCATION: (67)
OTHER INFORMATION: n equals a,t,9, or c
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Matches 994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Rosen et al.
TITLE OP INVENTION: Nucleic Acids, Proteins
FILE REFERENCE: PA106
                                                                                                                                                                                                                                                                                                                                      Local Similarity
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              CCCAGACTGCCCCCTGCCTGTTGCCCCCTGAGCCCACCTACTGCTCCAGATCGTGCAACT
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GTCCAGGAAGCCCTGGCCGTGCTGGAGCCCTAYGCGCGGCTGCCCCCCCACAAGCATGTG
                                                                   CGGGCCTACCGGGCCCTGCACTGCCCTACAGGCACTGAGTATACCCTGCAAGGTGTACCCC
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92.6%;
                                                 - CCTGCACTGCCCTACAGGCACTGAGTATACCTGCAA - GTGTACCCC
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Pred. No. 1e-221;
3; Mismatches
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GENERAL INFORMATION:

APPLICANT: Williams, Lewis T.

APPLICANT: Escobedo, Jaime
APPLICANT: Escobedo, Jaime
APPLICANT: Escobedo, Jaime
APPLICANT: Honis, Michael A.

APPLICANT: Garcia, Pablo Domini
APPLICANT: Sudduth-Kiliger, Jul
APPLICANT: Reinhard, Christoph
APPLICANT: Reinhard, Christoph
APPLICANT: Randazzo, Filippo
APPLICANT: Randazzo, Filippo
APPLICANT: Kennedy, Giulia C.
APPLICANT: Kennedy, Giulia C.
APPLICANT: Lamson, George
APPLICANT: Lamson, George
APPLICANT: Crkvenjakov, Radomir
APPLICANT: Dickson, Mark
APPLICANT: Dickson, Mark
APPLICANT: Labat, Ivan
APPLICANT: Labat, Ivan
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US-09-003-719-519
/ Sequence 519, Application US/09803719
/ Publication No. US20030044783A1
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    Drmanac, Snezana
Labat, Ivan
                                                                                                                                                 Escobedo, Jaime
Innis, Michael A.
Garcia, Pablo Dominiguez
Sudduth-Klinger, Julie
Reinhard, Christoph
Giese, Klaus
                                                                                                                                                                                                                                                                                                                                                                                                             CCCTTAGCCCCAACCCGATCCCATCTCTGGGAGGCTGCCCAGGTGGTCCCTGATGGACTG
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                                                    Lamson, George
Drmanac, Radoje
Crkvenjakov, Radomir
Leshkowitz, Dena
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APPLICANT: Kita, David

APPLICANT: Garcia, Veronica

APPLICANT: Jones, Lee William

APPLICANT: Stache-Crain, Birgit

TITLE OF INVENTION: Human Genee and Gene Prod

PILE REFERENCE: 1624.002

CURRENT APPLICATION NUMBER: US/09/803,719

CURRENT FILING DATE: 2001-03-09

PRIOR APPLICATION NUMBER: 60/188,609

PRIOR FILING DATE: 2000-03-09

INUMBER OF SEQ ID NOS: 2396

SOPTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 519

LENGTH: 396

TYPE: DNA

ORGANISM: Homo sapiens

US-09-803-719-519
PRIOR APPLICATION NUMBER: 09/693,267
PRIOR FILING DATE: 2000-10-20
PRIOR PRIOR APPLICATION NUMBER: 09/65,363
PRIOR PRIOR DATE: 2000-09-19
PRIOR APPLICATION NUMBER: 09/516,847
PRIOR APPLICATION NUMBER: 09/596,193
PRIOR APPLICATION NUMBER: 09/574,454
PRIOR PRIOR PRIOR DATE: 2000-06-17
PRIOR APPLICATION NUMBER: 09/574,454
PRIOR PRIOR PRIOR DATE: 2000-05-19
PRIOR PRIOR PRIOR NUMBER: 09/519,705
PRIOR PRIOR DATE: 2000-03-07
NUMBER OF SEQ ID NOS: 752
SEQ ID NO 116
LENGTH: 1909
TYPE: DNA
ORGANIEM: Homo Bapiens
PEATURE:
NAME/KEY: CDS
LOCATION: (135)..(941)
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US-10-291-172-116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 116, Application US/10291172 Publication No. US20030228584A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 26.3
Best Local Similarity 97.3
Matches 287; Conservative
                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NO. US20030228584A1e1
FILE REPERENCE: 21272-045
CURRENT APPLICATION NUMBER: US/10/291,172
CURRENT FILING DATE: 2000-11-08
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Sequence 73, Application US/10119926
Publication No. US20030104413A1
GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Zhang, Jie
APPLICANT: Zhang, Jie
APPLICANT: Zhao, Ging A.
APPLICANT: Chen, Rui-hong
APPLICANT: Chen, Rui-hong
APPLICANT: Wehrman, Tom
APPLICANT: Shou, Ping
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Best Local Similarity 60.7%;
Matches 447; Conservative
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Pred. No. 1.2e-59;
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APPLICANT: Yang, Yonghong
APPLICANT: Xue, Aidong J.
APPLICANT: Xue, Aidong J.
APPLICANT: Xue, Aidong J.
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. US2003004413A1el Nucleic Aci
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 789C1P2BCON
CURRENT FILING DATE: 2002-04-09
FRICH APPLICATION NUMBER: US/10/119,926
CURRENT FILING DATE: 2000-05-19
FRICH APPLICATION NUMBER: 09/574,454
PRICH APPLICATION NUMBER: 09/519,705
FRICH APPLICATION NUMBER: 09/519,705
FRICH FILING DATE: 2000-03-07
NUMBER OF SEQ ID NOS: 108
SOFTWARE: pt PL_genes Version 1.0
SEQ ID NO 73
IRRCTH: 1909
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ORGANISM: Homo sapi
FEATURE:
INAMS/KEY: CDS
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Pred. No. 1.2e-59;
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APPLICANT: Sues Stuart
APPLICANT: Jed G. Nuchtern
APPLICANT: Sharon E. Plon
APPLICANT: Jason M. Shohet
TITLE OF INVENTION: GENES REGULATED BY MYCN
FILE REFERENCE: PA-0046 US
CURRENT APPLICATION NUMBER: US/10/084,817
CURRENT PILING DATE: 2002-02-25
PRIOR APPLICATION NUMBER: 60/270,784
PRIOR APPLICATION NUMBER: 60/270,784
PRIOR FILING DATE: 2001-02-23
NUMBER OF SEQ ID NOS: 365
SOFTWARE: PERL PROGRAM
SEQ ID NO 300
LENGTH: 4336
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; OTHER INFORMATION: Incyte
US-10-084-817-300
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US-10-084-817-300
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ORGANISM: Homo sapiens
FEATURE:
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RESULT 10
US-10-044-090-269
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CURRENT APPLICATION NUMBER: US/10/044,090
CURRENT FILING DATE: 2002-01-09
NUMBER OF SEQ ID NOS: 850
SOPTWARE: PERL Program
SEQ ID NO 269
LENGTH: 3280
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 269, Application US/10044090 Publication No. US20020137081A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Olga Bandman
TITLE OF INVENTION: GENES DIFFERENTIALLY EXPRESSED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Homo sapiens FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: Incyte ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAMB/KEY: misc_feature
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AAGCCGCCACCGTATCCCTGAGGCTGAGGCTGCCGTGCTCTTCCGCCAGATGGCCACCGC
                                                                                                                       TACCCAGCTCCTCTACGCCTTTTTCACTCGGACCATGGGGACATGCACAGCCTGGTGCG
                                                                                                                                                                                                                             CAGCGGAGAGGAGCTGGTGCAAGGTGTTTGATATCAGCTGCTACCAGGAATCCCTGGC 582
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                                                                              TGAGACCAAAGCCTATGTGTTCTTTGAGCGAACGTATGGGGAACATGCATTCCTTCGTCCG
                                                                                                                                                                              ACCGTGCTTTTTGCCTGTCTGCTCATAGTAACATCAACCAAATCACTGAAATTATCCTGGG
                                                                                                                                                                                                                                                                                                                             TACAGGCACTGAGTATACCTGCAAGGTGTACCCCGTCCAGGAAGCCCTGGCCGTGCTGGA 326
                                                                                                                                                                                                                                                                                                                                                                              GAMATACTTATTGTTGGAACCTCTGGAGGGAGACCACGTTTTTCGTGCCGTGCATCTGCA
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Pred. No. 1.6e-56;
0; Mismatches 386
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APPLICANT: INCYTE GENOMICS, INC.
APPLICANT: SHIFFMAN, DOV
APPLICANT: SHIFFMAN, DOV
APPLICANT: SHIFFMAN, DOV
APPLICANT: SHIFFMAN, Jeffrey J.
APPLICANT: SEILHAMER, Jeffrey J.
APPLICANT: PORTER, GORDON J.
APPLICANT: MIKITA, Thomas
APPLICANT: MIKITA, Thomas
APPLICANT: MIKITA, Thomas
APPLICANT: MIKITA, Thomas
APPLICANT: NAI, Julie
TITLE OF INVENTION: GENES EXPRESSED IN FOAM
PILE REFERENCE: PA-0025 PCT
CURRENT APPLICATION NUMBER: US/10/240,965
CURRENT APPLICATION NUMBER: 60/195,106
PRIOR APPLICATION NUMBER: 60/195,106
PRIOR FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 276
SOPTWARE: PERL PROGram
SEQ ID NO 168
LENGTH: 3324
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Publication No. US20
GENERAL INFORMATION:
             FEATURE:
NAME/KEY: unsure
LOCATION: 254, 378
OTHER INFORMATION:
                                                                               FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte
                                                                                                                                           TYPE: DNA
ORGANISM: Homo sapiens
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Best Local Similarity
Matches 400; Conserv
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                                 GTCGGGAGCCAGCTGAACGGCTCACAGCCACAGGCATCCTCCTGCACCCCCTGGCT 944
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                                                                  AGTTCTGCATTCCTGAGCACATTTCCCCCCAAAGCCAGGTGCCTCATTCGCAGCCTCTTGA
                                                                                                                                                                                                                          ACTCGGGCAAGGCAGCCGATGTCTGGAGCCTGGGCGTGGCGCTCTTCACCATGCTGGCCG
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Pred. No. 2
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RESULT 12

US-10-228-263-1

Sequence 1, Application US/10228263

Publication No. US20030099985A1

APPLICANT: LI, Jing

ITILE OF INVENTION: AMPLIFIED GENE INVOLVED IN CANCI

FILE REFERENCE: 38002-0034

CURRENT APPLICATION NUMBER: US/10/228,263

CURRENT FILING DATE: 2002-12-04

PRIOR APPLICATION NUMBER: US 60/330,797

PRIOR APPLICATION NUMBER: US 60/314,655

PRIOR FILING DATE: 2001-00-31

PRIOR APPLICATION NUMBER: US 60/314,655

PRIOR FILING DATE: 2001-08-27

NUMBER OF SEQ ID NOS: 14

SOFTWARE: Patentin version 3.1

SEQ ID NO 1

LENGTH: 818

TYPE: DNA

ORGANISM: Homo sapiens

FRATURE:

NAME/KEY: misc feature

LOCATION: (788). . (788)

OTHER INFORMATION: N can be C or T
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Sequence 3, Application US/10228263

Publication No. US20030099985A1

GENERAL INFORMATION:
APPLICANT: LI, Jing
TITLE OF INVENTION: AMPLIFIED GENE INVOLVED IN CANCER
FILE REFERENCE: 38002-0034

CURRENT APPLICATION NUMBER: US/10/228,263

CURRENT FILING DATE: 2002-12-04

PRIOR APPLICATION NUMBER: US 60/330,797

PRIOR APPLICATION NUMBER: US 60/330,797

PRIOR APPLICATION NUMBER: US 60/314,655

PRIOR APPLICATION NUMBER: US 60/314,655

PRIOR APPLICATION NUMBER: US 60/314,655

PRIOR PILING DATE: 2001-08-27

NUMBER OF SEQ ID NOS: 14

SOPTWARE: PATENTIN VETBION 3.1

SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; FEATURE:
; NAME/KEY: CDS
; LOCATION: (56)..(67
; OTHER INFORMATION:
US-10-228-263-1
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US-10-228-263-3
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US-10-228-263-3
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Best Local
             LENGTH: 621
TYPE: DNA
ORGANISM: Homo
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; OTHER INFORMATION: n equals a,t,g, US-09-925-301-525
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US-09-925-301-525
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                                                                                                                                                                                                                                                                                                                                                            Sequence 525, Application US/09925301
Patent NO. US20020053308A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins
FILE REFERENCE: PA106
CURRENT APPLICATION NUMBER: US/09/925,301
CURRENT FILING DATE: 2001-08-10
                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 1694
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 525
                           ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (515)
OTHER INFORMATION: n equals a
NAME/KEY: misc_feature
LOCATION: (526)
OTHER INFORMATION: n equals a
NAME/KEY: misc_feature
LOCATION: (526)
OTHER INFORMATION: n equals a
NAME/KEY: misc_feature
LOCATION: (557)
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Best Local Similarity
Matches 332; Conserv
                                                                                                                                                                                                                                                                                      CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05882
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SECTION NUMBER: 60/124,270
NUMBER OF SEC
                                                                                                                                                                                                         LENGTH: 56
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CGCCAGATGGCCACCGCCCTGGCGCACTGTCACCAGCACGGTCTGGTCCTGCGTGATCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTCACAGCCACAGGCATCCTCCTGCACCCCTGGCT 944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAGCTTAGGAAGTTCGTCTTCTCCACGGAGAGAGAACCCAGCTTAGACTAGAAAGTCTA
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                                                                                                                  a,t,g,
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Pred. No. 7.2e-49;
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APPLICANT: HYGORITON: NO. US20030228584A1el Nucleic Acids and Polypeptides
TITLE OF INVENTION: NO. US20030228584A1el Nucleic Acids and Polypeptides
FILE REFERENCE: 21272-045
FILE REFERENCE: 21272-045
CURRENT APPLICATION NUMBER: US/10/291,172
CURRENT APPLICATION NUMBER: US/10/291,172
CURRENT FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-09-65,363
PRIOR FILING DATE: 2000-09-14
PRIOR FILING DATE: 2000-09-14
PRIOR PRIOR PILING DATE: 2000-09-19
PRIOR PILING DATE: 2000-09-17
PRIOR APPLICATION NUMBER: US/596,193
PRIOR APPLICATION NUMBER: US/5974,454
PRIOR APPLICATION NUMBER: US/519,705
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US-10-291-172-492
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// TYPE: DNA
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US-10-291-172-492
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Best Local Similarity 60.2%;
Matches 396; Conservative
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LENGTH: 1943
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Pred. No. 1.7e-48;
5; Mismatches 4
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                                                                                                                                        CCGGCCACTACCCCTTCCAGGACTCGGAGGCCTGTCCTGCTCTTCGGCAAGATCCGCCGCG 826
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                                                                                                                        TGGGACGATACCCCTTCCATGACTCAGACCCCCAGTGCCCTTTTCTCCAAAATTCGGCGTG
TGAGACGGGAGCCCTCCGAGAGACTCACTGCCCCCGAGATCCTACTGCACCCCTGGTT
                              TTCGTCGGGAGCCAGCTGAACGGCTCACAGCCACAGGCATCCTCCTGCACCCCTGGCT 944
                                                            GACAGTTCTGCATTCCTGAGCACATTTCCCCCCAAAGCCAGGTGCCTCATTCGCAGCCTCT
                                                                                        GGGCCTACGCCTTGCCTGCAGGCCTCTCGGCCCCTGCCCGCTGTCTGGTTCGCTGCCTCC 886
                                                                                                                                                                                 TACTCCGGAAAGGCTGCGGACGTTTGGACTGGGGGGGGGTGATGCTCTACACCCTTCTGGT
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Search completed: January 16, 2004, 20:19:10 Job time: 373.799 secs

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Maximum Match 100%
Listing first 45 summaries
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     Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                       956
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Match
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1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*

2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*

3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*

4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*

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US-09-136-421-4
US-08-146-421-4
US-08-913-050A-2
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US-09-691-861A-14
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US-09-691-861A-13
US-09-691-861A-20
US-09-691-861A-3
US-09-691-694-133
US-09-691-694-133
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US-08-459-504B-20
US-08-459-504B-20
US-08-459-504B-20
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US-08-557-006C-38
US-08-557-006C-39
US-08-557-006C-39
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Sequence 3, Appli
Sequence 4, Appli
Sequence 2, Appli
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Sequence 1146, Ap
Sequence 391, Appli
Sequence 391, Appli
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Sequence 20, Appli
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Matches	PLI -50	44440000000000000000000000000000000000
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CAGGAA	902A-3 3, Application US/0 0. 6387676 INFORMATION: INFORMATION: TINFORMATION: MT: Mird, Timothy A MT: Marken, John S. FINURNTION: Human FERRENCE: 2877-US APPLICATION NUMBER: FILING DATE: 1995- OF SEQ ID NOS: 16 E: Patentin Ver. 2. 0 3 E: 1085 DNA SM: Homo Bapiens 902A-3	44444400000000000000000000000000000000
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Similarity 99.9%; Pred. No. 3.2e-207; Conservative 0; Mismatches 1; Indels 0; Gaps ATGCGAGCCACCCTCTGGCTGCTCCTGCGGGTTCCCTGTCCAGGAAGAAGCGGTTGGAG ATGCGAGCCACCCCTCTGGCTGCTCCTGCGGGTTCCCTGTCCAGGAAGAAGCGGTTGGAG ATGCGAGCCACCCCTCTGGCTGCTCCTGCGGGTTCCAGAAACCAGCTTGGAG TTGGATGACAACTTAGATACCGAAGCGTCCCAGAAACCAGCTCCAGAAACCAGCTTGGAG TTGGATGACAACTTAGATACCGAGCGTCCCGTCC	, g	
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                                                                                                                                                                                    / LENGTH: 2559
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-220-132-135
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US-09-220-132-135/c
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SOPTWARE: FABLE
SEQ ID NO 135
FORGTH: 2559
                                                                                                                                                                                                                                                                            Sequence 135, Application US/09220132

Patent NO. 6506607

GENERAL INFORMATION:
APPLICATTI Shyjan, Andrew W.
APPLICATTINE OP INVENTION: METHODS AND COMPOSITONS FOR THE IDENTIFICATION AND ASSESSMENT
TITLE OP INVENTION: OF PROSTATE CANCER THERAPIES AND THE DIAGNOSIS OF PROSTATE CANCE
FILE REFERENCE: 07334-074001
CURRENT APPLICATION NUMBER: US/09/220,132
CURRENT APPLICATION NUMBER: US 60/079,303

PRIOR APPLICATION NUMBER: US 60/068,821
PRIOR APPLICATION NUMBER: US 60/068,821
PRIOR PILING DATE: 1998-12-24
NUMBER OF SEQ ID NOS: 191
SOFTWARE PRACES FOR SEC 11-11
                                                                                                                                    Query Match 39.7%;
Best Local Similarity 93.8%;
                                                     1634
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                                                   TGACCCTTCTGTTTCTCCCCATGTCCCAGGAAGAAGCTGGTGCTGGAGAACCTGGAGAAGAC
TCCTGCGTGCTGACTGGGCCAGATGATTCCCTGTGGGACAAGCACGCGTGCCCAGCCTAC
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                                                                                                                      Conservative
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                                                                                                                    Score 426.2; DB 4;
Pred. No. 1.7e-87;
0; Mismatches 28;
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                                             CORRESPONDENCE ADDRESSE: DILMORTH & BARRESE STRESE: 4350 LA JOLLA VILLAGE DRIVE, CITY: SAN DIEGO STATE: CALIFORNIA COUNTRY: U.S.A.
ZIP: 92122
COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PATENTIN Release #1.0, Ver CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/146,421 FILING DATE: 29-OCT-1993
CLASSIFICATION HOMBER: US/08/146,421 FILING DATE: 29-OCT-1993
CLASSIFICATION NUMBER: 489-2
REGISTRATION NUMBER: 489-2
TELEPHONE: 619-546-4410
TELEPHONE: 619-546-4410
TELEPHONE: 619-545-2839
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 2562 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
TOPOLOGY: linear
TOPOLOGY: linear
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US-08-146-421-4/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: BREWER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: BREWER, GARY
TITLE OF INVENTION: DNA SEQUENCE ENCODING A
TITLE OF INVENTION: ANTI-TUMOR PROPERTIES
NUMBER OF SEQUENCES: 9
                               MOLECULE TYPE:
FEATURE:
NAME/KEY:
LOCATION:
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Patent No. 5827726
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Best Local Similarity
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                                                                                                                                                                                                                                                                               TITLE OF INVENTION: DNA NUMBER OF SEQUENCES: 10 CORRESPONDENCE ADDRESS: ADDRESSEE: BROWNY ****
                                                                                  COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM FC comparible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Veri
CURRENT APPLICATION DATA:

APPLICATION UMBER: US/08/913,050A

PILING DATE: 05-SEP-1997

PRIOR APPLICATION DATA:

APPLICATION DATA:

APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                       APPLICANT: NEZU,
                APPLICATION NUMBER: JP 57104/1995
FILING DATE: 16-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP PCT/JP96/00660
FILING DATE: 15-MAR-1996
                                                                                                                                                                                                                                                   STREET: 41
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93.8%;
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pred. No. 1.7e-87;
0; Mismatches 28;
                                                                                                                                                 Version
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197
TELEPAX: (202) 737-3528
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1302 base pairs
TYPE: nucleic acid
cre and controlled acid
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Best Local S
Matches 241
                                                                                                                                                                                       Sequence 1146, Application US/09016434 Patent No. 6500938
                                                                                                         GENERAL INFORMATION:
APPLICANT: Janice Au-Young
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION
TITLE OF INVENTION: PATHWAY GENE EXPRESSION
          STREET: 31/3
CITY: PALO ALTO
CTATE: CALIFORNIA
                                                                                 NUMBER OF SEQUENCES: 1
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Local Similarity 48.1%;
hes 241; Conservative
                                                                    ADDRESSEE:
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SIGNALING

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557 CCGGTGGCACCCTCAAAATCTCCGACCTGGGCGTGGCCGAGGCACTGCACCCGTTCGCGG
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TICGCIGCCICCITCGICGGGAGCCAGCIGAACGGCICACAGCCACAGGCAICCICCIGC 934
                                                                                                                                                              AGATCCGCCGCGGGGCCTACGCCTTGCCTGCAGGCCTCTCGGCCCCTGCCCGCTGTCTGG
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                                                                               ACATCGGGAAGGGAGCTACGCCATCCCGGGCGACTGTGGCCCCCCGCTCTCTGACCTGC
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Pred. No. 1.5e-10;
0; Mismatches 260;
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US-09-016-434-1146
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REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0(
TELECOMMUNICATION: INFORMATION:
TELEPHONE: (650) 855-0555
TELEPHONE: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1146:
SEQUENCE CHARACTERISTICS:
LENGTH: 1302 base pairs
TYPE: nucleic acid
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Best Local :
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,434
FILING DATE: HEREWITH
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MEDIUM
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IMMEDIATE SOURCE:
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Local Similarity 48.1%;
nes 241; Conservative
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CLASSIFICATION:
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                                                                           ACCCCTGGCTGCGACAGGACC 955
                                                                                                                                          TICGCTGCCTTCGTCGGGAGCCAGCTGAACGGCTCACAGCCACAGGCATCCTCCTGC 934
                                                                                                                                                                           ACATCGGGAAGGGGAGCTACGCCATCCCGGGCGACTGTGGCCCCCCGCTCTCTGACCTGC
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                                              ACAGCTGGTTCCGGAAGAAAC 937
                                                                                                             TGAAAGGGATGCTTGAGTACGAACCGGCCAAGAGGTTCTCCATCCGGCAGATCCGGCAGC
                                                                                                                                                                                                                                                                                                         ACGGCCTGGACACCTTCTCCGGCTTCAAGGTGGACATCTGGTCGGCTGGGGTCACCCTCT
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Pred. No.
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LENGTH: 1466 ban Type
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Patent No. 5985635
GENERAL INFORMATION:
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Best Local Similarity
Matches 237; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Bandman, Olga
APPLICANT: Goli, Surya K.
APPLICANT: Hilman, Jennifer L.
TITLE OF INVENTION: NOVEL HUMAN SERINE/THREONINE
TITLE OF INVENTION: PROTEIN KINASES
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOPTWARE: FABLEBQ Version 2.0 CURRENT APPLICATION DATA; APPLICATION UNMBER: US/08/749, FILING DATE: Filed Herewith PRIOR APPLICATION UMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION: TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF
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OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
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CITY: Palo Alto
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ACAACATCACCACGGGTCTGTACCCCTTCGAAGGGGGACAACATCTACAAGTTGTTTGAGA
                               TCACCATGCTGGCCGCCACTACCCCTTCCAGGACTCGGAGCCTGTCCTGCTCTTCGGCA
                                                              ACGGCCTGGACACCTTCTCCGGCTTCAAGGTGGACATCTGGTCGGCTGGGGTCACCCTCT
                                                                                          GCTCACGGGCCTCATACTCGGGCAAGGCAGCCGATGTCTGGAGCCTGGGCGTGGCGCTCT
                                                                                                                           CGGACGACACCTGCCGGACCAGCCAGGGCTCCCCGGCTTTCCAGCCGCCCGANATTGCCA
                                                                                                                                                       CAGATGATTCCCTGTGGGACAAGCACGCGTGCCCAGCCTACGTGGGACCTGAGATACTCA
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Pred. No. 9.1e-10;
0; Mismatches 264;
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US-09-016-434-391
; Sequence 391 Application US/09016434
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                                                                                                                                                                                              US-09-016-434-391
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6...
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016.474
PILING DATE: HEREWITTER
                                                                                                                                                Query Match
Best Local
                                                                                                                               Matches
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APPLICANT: Jeffrey J. Seilhamer
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
TITLE OF INVENTION: PATHWAY GENE EXPRESSION
                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                        TOPOLOGY: line
                                                                                                                                                                                                                                                                                                                                                                      NAME: Zeller, Karen J.
REGIZATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION: NAME: Zeller, Karen J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                           LIBRARY: BRAITUT03
CLONE: 2108752
                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
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STATE: CALIFORNIA
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                                                                                                                                            Similarity 63.3%;
CCGTACCGTGGCAAGCCCAGTGACATGTGGGCCCTGGGCGTGGTGCTCTTCACCATGCTG
                                TCATACTCGGGCAAGGCGATGTCTGGAGCCTGGGCGTGGCGCTCTTCACCATGCTG
                                                                                               CTGTGGGACAAGCACGCGTGCCCAGCCTACGTGGGACCTGAGATACTCAGCTCACGGGCC 705
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                                                              CTGAAGGACCAGAGAGGGAGCCCTGCCTACATCAGTCCCGACGTGCTCAGCGGCCGG----
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                                                                                                                             Score 71; DB 4;
Pred. No. 1.7e-07;
D; Mismatches 70
                                                                                                                          70;
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US-09-016-434-1147
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US-09-016-434-1147
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Matches 31
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Patent No. 6500938
                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (650) 855-
TELEFAX: (650) 845-41
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:

NAME: Zeller, Karen J.

REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL
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CURRENT APPLICATION NUMBER: US/09/016 47'
FILING DATE: HERESTER: US/09/016 47'
CLASSIPTATE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Janice Au-Young
APPLICANT: Jeffrey J. Seilhamer
TITLE OP INVENTION: COMPOSITION F
TITLE OP INVENTION: PATHWAY GENE
                                                                                                                                                                                                                                                                                              IMMEDIATE SOURCE:
LIBRARY: GENBANK
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PRIOR APPLICATION DATA:
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TOPOLOGY: lir
                                                                                                                                                                                                                                                                                                                                                           LENGTH: 2169 base pairs
TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                 276
336 GGAGCTCTGCAGCCGAAAGTCCCTGGCCCACATCTGGAAGGCCCGGCACACCCTGTTGGA
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                                                                                              348 GCACAAGCATGTGGCTCGGCCCACTGAGGTCCTGGCTGGTACCCAGCTCCTCTACGCCTT 407
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                                                                                                                                                                                               6.1%; al Similarity 45.9%; 310, Conservative
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: CALIFORNIA
                             TTTCACTCGGACCCATGGGGACATGCACAGCCTGGTGCGAAGCCGCCACCGTATCCCTGA 467
                                                              CCGCCACATCGTGCGTTTTTCGCACCACTTTGAGGACGCTGACAACATCTACATTTTCTT
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3174 PORTER DRIVE
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                                                                                                                                                                                               Score 65.6; DB 4;
Pred. No. 4e-06;
0; Mismatches 354;
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US-09-579-664B-4
                                                                                                                                                                                                                                                                   US-09-579-664B-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Immunex Corporation
APPLICANT: Bird, Timothy A.
APPLICANT: Virca, G. Duke
APPLICANT: Wartin, Unja
                                                                                                                                                                                                               Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                  SOPTWARE: PatentIn version 3.1
SEQ ID NO 4
LENGTH: 2902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 4, Application US/09579664B Patent No. 6514719
                                                                                                                                                                                              Matchee
                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Anderson, Dirk M.

TITLE OF INVENTION: NOVEL MURINE AND HUMAN KINASES
FILE REPERENCE: 2923-A
CURRENT APPLICATION NUMBER: US/09/579,664B
CURRENT FILING DATE: 2000-05-26
NUMBER OF SEQ ID NOS: 36
                                                                                                                                                                                                                                                                       LENGTH: 2902
TYPE: DNA
ORGANISM: Mus musculus
                                                                                                                                                                                            Match 5.1%;
Local Similarity 49.7%;
Lee 231; Conservative
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GCTGACCGTGAGAGGAAGGAAGCTGGTGCTGGAGAACCTGGAGGACTCCTGCGTGCTGACT
                                                                          GCGCACTGTCACCAGCACGGTCTGGGTCCTGCGTGAGCTGAGCTGTGTCGCTTTGTCTTC
                                                    CACTACTGCCACCAGAACGGGATCGTTCACCGAGATCTCAAGCTGGAAAACATCCTTCTA
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                                                                                                                       COGCCACOGCTGAGCGGGACGCCAGGCATTTCTTCCGACAGATCGTGTCTGCCCTG
                                                                                                                                                         CGCCACCGTATCCCTGAGCCTGAGGCTGCCGTGCTTCCGCCAGATGGCCACCGCCCTG
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    GGCCCTGAAGCGGATGTATGGTCACTGGGCTGTGTCATGTACACGCTGCTCTG

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                                                                                                                                                                                           Score 54.6; DB 4; Length 29
Pred. No. 0.0013;
0; Mismatches 219; Indels
                                                                                                                                                                                                                              Length 2902;
                                                                                                                                                                                            15;
                                                                                                                                                                                           Gaps
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RESULT 10
US-08-125-468-1/c
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                                                                      US-08-125-468-1
                Query Match
Best Local
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GENERAL INFORMATION:
     Matches
                                                                                                                                                               INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Ryan, Michael J.
APPLICANT: Lotvin, Jason A.
APPLICANT: Strathy, Nancy
APPLICANT: Fanting
                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Fantini, Susan E.
TITLE OF INVENTION: Cloning of the biosynthetic pathway for
TITLE OF INVENTION: chlortetracycline and tetracyline formation and cosmids
TITLE OF INVENTION: useful therein
NUMBER OF SEQUENCES: 1
                                                                                                                                                                                                                           REGISTRATION NUMBER: 31,145
REFERENCE/DOCKET NUMBER: 31.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201)831-3241
                                                                                     TOPOLOGY: 1: MOLECULE TYPE:
                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Tsevdos, Estelle J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                     STRANDEDNESS: single
                                                                                                                                         TYPE:
                                                                                                                                                        LENGTH:
                                                                                                                                                                                                                                                                                                                                FILING DATE: 22-SEP-1993
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
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                   Similarity
                                                                                                                                    H: 30001 base pairs nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New Jersey
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                                                                                                                                                                                                          (201)831-3305
 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               American
                                                                                   (genomic)
                  44.2%;
                                                                                                                                                                                                                                                                                                                                                                    US/08/125,468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cyanamid Company
Score 51.2; DI
Pred. No. 0.01:
0; Mismatches
 <u>.</u>
                                                                                                                                                                                                                                                               255-02
                                                                                                                                                                                                                                                                                                                                                                                                     Version #1.25
                  .011,
                              1.
                                  Length 30001;
 Indels
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390 CCAGCTCCTCTACGCCTTTTTCACTCGGACCCATGGGACATGCACAGCCTGGTGCGAAG

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RESULT 11
US-08-474-933-1/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1, Applic
Patent No. 5866410
                                                           CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/125,468
PILING DATE: 22-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: TBEVEGO, ESTELLE J
REGISTRATION NUMBER: 31,145
REPERENCE/DOCKET NUMBER: 31,255-02
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Ryan, Michael J.
APPLICANT: Lotvin, Jason A.
APPLICANT: Strathy, Nancy
APPLICANT: Strathy, Nancy
APPLICANT: Pantini, Susan E.
TITLE OF INVENTION: Clioning of the biosynthetic pathway for
TITLE OF INVENTION: chlortetracycline and tetracyline Formation
                INFORMATION FOR SEQ ID NO
                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/474,93: FILING DATE:
                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIDM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: American Cyanamid Company
BEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
                                                  TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Wayne
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CHARACTERISTICS
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; TOPOLOGY: linear
; MOLECULE TYPE: DNA (ger
US-08-474-933-1
                                                           US-09-691-861A-14
                                                                                                                                                                                                                                                                                                                                                              US-09-691-861A-14
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                                                                                                                                                                                                                                                                                                                 Sequence 14, Application US/09691861A Patent No. 6482935
GENERAL INFORMATION:
                Query Match
Best Local
                                                                                                                                                                          SEQ ID NO 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 212; Conserv
     Matches
                                                                                                                                                                                                  APPLICANT: Wei, Ming-Hui et al.
TITLE OF INVENTION: ISCLATED HUMAN KINASE PROTEINS,
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN
TITLE OF INVENTION: THEREOF
FILE REFERENCE: CL000892
CURRENT FILLING DATE: 2000-10-18
CURRENT FILLING DATE: 2000-10-18
NUMBER OF SEQ ID NOS: 22
                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 22
SOFTWARE: PastSEQ for Windows
                                                                      NAME/KEY: misc_feature LOCATION: (1)...(601)
OTHER INFORMATION: n =
                                                                                                                 LENGTH: 601
TYPB: DNA
ORGANISM: Homo sapiens
FEATURE:
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Score 51; DB 4;
Pred. No. 0.0062;
0; Mismatches 18
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                             DB 4;
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181,
                          Length 601
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FILE REPRENCE: CLOORSE

FULE REPRENCE: CLOORSE

CURRENT APPLICATION NUMBER: US/09/691,86

CURRENT FILING DATE: 2000-10-18

NUMBER OF SEQ ID NOS: 22

SOPTWARE: FABLSEQ for Windows Version 4.

SEQ ID NO 1

LENGTH: 1104

TYPE: DNA

ORGANISM: Homo sapiens

US-0:9-691-861a-1
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US-09-691-861A-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/09691861A
Patent No. 6482935
GENERAL INFORMATION:
APPLICANT: We1, Ming-Hui et al.
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS,
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS,
TITLE OF INVENTION: THEREOF
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Best Local Similarity
Matches 188, Conserv
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                         CTTCTGTGGGTCACCAGCGTATGCGGCCCCAGAGGTGCT---GCAGGGCATTCCCTACCA
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llarity 49.7%;
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Pred. No. 0.0095;
0; Mismatches 181;
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                                Sequence 536 Application US/09016434
Patent No. 6500338
GENERAL INFORMATION:
APPLICANT: Janice Au-Young
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FO
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NUMBER OF SEQUENCES: 1 CORRESPONDENCE ADDRESS: ADDRESSEE: INCYTE PH

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US/09016434

PHARMACEUTICALS,

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APPLICANT; Wei, Ming-Hui et al.
APPLICANT; Wei, Ming-Hui et al.
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND ITITLE OF INVENTION: THEREOF
FILE REFERENCE: CL000892
CURRENT APPLICATION NUMBER: US/09/691,861A
CURRENT FILING DATE: 2000-10-18
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 9862
TYPE: DNA
ORGANISM: Homo sapiens
RESULT 15
US-09-016-434-536
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COUNTRY: USA

ZIP: 94304

COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,434
FILING DATE: HEREWITH
CLASSIFICATION INVBER:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 37,071
REFILING DATE:
CLASSIFICATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REGISTRATION NUMBER: PA-0002 US
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPAX: (650) 855-0555
TELEPAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 536:
SEQUENCE CHARACTERISTICS:
LENGTH: 263 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TYPE: nucleic acid
STRANDEDNESS: single
ILBRARY: NGANNOTO1
CLONE: 2314392
US-09-016-434-536
Search completed: January 16, 2004, 16:49:45 Job time : 72.5605 secs
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1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*

2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*

3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*

4: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*

5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*

6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*
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US-09-509-902A-3
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US-08-131-050A-2
US-09-913-050A-2
US-09-959-023-1
US-09-959-023-300
US-09-996-243-300
US-09-996-243-245
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US-09-316-536-66
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	CCCTGCACTGCCCTACAGGCACTGAGTATACCTGCAAGGTGTACCCCGTCCAGGAAGCC	CCCTGCCTGTTGCCCCTGAGCCCACCTACTGCTCCAGATCGTGCAACTGCTGTGGCCACTACTGCTGCTGCTGCTGTGGCCACTACTGCTGCTGGAGCCGAGGAGGGGGGGG	TAGATACCGAGCGTCCCGTCCAGAAACGAGCTCGAAGTGGGCCCAGCCCAGCCCAGACTGCCC CCTGCCTGTTGCCCCTGAGCCCACCTACTGCTCCAGATCGTGCAACTGCTGTGGCAACT	TTAGATACCGAGCGTCCCGTCCAGAAACGAGCTCGAAGTGGGCCCCAGCCCCAGCCTGCCC	CCTCTGGCTGCTCCTGCGGGTTCCCTGTCCAGGAAGAAGCGGTTGGAGTTGGATGACAAC	GCTCTGAGCCCCGGCGGCCCCGGGCCCACGCGGAACGACGGGGCGAGATGCGAGCCACC	tch al Similarity 1005; Conservat	icati 76 76 76 100: 100: 100: 100: 100: 100: 100: 100		3
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	GAGT	CTCC	CCTAC	 	C161	6—60 6—60 6—60	Score 1004. Pred. No. 4 0; Mismatch	1. DNAS Encoding US/09/509,902A	al i gnment	
	TACC	regae IIIIII	HECT HECT	JAGCT	CCAGG	ACGCG	e 6	ng Po 02A	ENTS	-417 -417 -7664 -7664 -243 -325 -325 -325 -335 -115 -115 -115 -273 -273 -273 -273
		CCCGA	CCAGA		AAGAJ AGAJ	GAACC	DB le-207	olypej		US-08-628-417-5 US-08-628-417-6 US-08-955-918C-1 US-08-697-766A-1 US-08-697-766A-1 US-09-461-325-128 US-09-461-325-128 US-09-465-558-59 US-09-014-969-14 US-09-248-335-27 US-09-248-335-27 US-09-602-877A-95 US-09-469-647-25 US-09-489-847-25 US-09-489-847-25 US-09-489-847-25
	6-161 	ATCGTK	TCGTC		6000 6000 6000 6000 6000 6000	ACGG	4	22A Encoding Polypeptides //509,902A		
	ACCC	GCGGG	CAAC CAAC	4222 	TIGGA	96067 	Lengt	8 Having		
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	360	300	240	18	120	139	0	Functions		2000 11 0
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Sequence 135, Application US/09220132

Sequence 135, Application:
GENERAL INFORMATION:
APPLICANT: Shyjan, Andrew W.
TITLE OP INVENTION: METHODS AND COMPOSITONS FOR THE IDENTIFICATION AND ASSESSMENT
TITLE OF INVENTION: OP PROSTATE CANCER THERAPIES AND THE DIAGNOSIS OF PROSTATE CANCE
FILE REFERENCE: 07334-074001
CURRENT APPLICATION NUMBER: US/09/220,132
CURRENT FILING DATE: 1998-12-23
PRIOR APPLICATION NUMBER: US 60/079,303
PRIOR APPLICATION NUMBER: US 60/079,303
PRIOR APPLICATION NUMBER: US 60/068,821
PRIOR APPLICATION NUMBER: US 60/068,821
PRIOR PILING DATE: 1997-12-24
NUMBER OF SEQ ID NOS: 191
SOPTMARE: PRASTSEQ for Windows Version 4.0
SEQ ID NO 135
LENGTH: 2559
TYPE: DNA
ORGANISM: Homo Sapiens
US-09-220-132-135
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US-09-220-132-135/c
                                             Query Match
Best Local Similarity
Matches 566; Conserv
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                                           24.5%;
llarity 94.6%;
Conservative
                                             0
                                           Score 505.2; DB 4;
Pred. No. 1.4e-99;
0; Mismatches 28;
                                             Indels
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                              US-08-146-421-4/c

| Sequence 4, Application US/08146421
| Patent NO. 5543499
| GENERAL INFORMATION:
| APPLICANT: BREWER, GARY
| TITLE OF INVENTION: DNA SEQUENCE ENCODING A PITTLE OF INVENTION: ANTI-TUMOR PROPERTIES
| NUMBER OF SEQUENCES: 9
| CORRESPONDENCE ADDRESS:
| ADDRESSEB: DILWORTH & BARRESE
| STREET: 4350 LA JOLLA VILLAGE DRIVE, SUITE: CALIFORNIA
| COUNTRY: U.S.A. ZIP: 92122
| COMPUTER: EAM PIEGO STATE: CALIFORNIA
| COUNTRY: U.S.A. ZIP: 92122
| COMPUTER: IBM PC COMPATALE
| COMPUTER: IBM PC COMPATALE
| COMPUTER: PEPPER PLD, PREDERICK W. REPLICATION DATA: APPLICATION DATA: APPLICATION INFORMATION: SOTTMATS: 29-OCT-193
| CLASSIFICATION NUMBER: US/08/146,421
| FILLING DATE: 29-OCT-193
| CLASSIFICATION NUMBER: 489-2
| TELECOMMUNICATION INFORMATION: TELEPRICATION INFORMATION: TELEPRICATION: 619-546-4410
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TELEFAX: 619-453-2839
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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1634 TGACCCTTCTGTTTCTCCCCATGTCCCAGGAAGAAGCTGGTGCTGGAGAACCTGGAGGAC
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                              AGGGAAGAGGAGGACAGAGAAGTGGTTCTGTATGGCTAGGACCACCCTACTACACGC 1143
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                                                                                                            AGGGAAGAGGAGAGAGAGAGTGGTTCTGTATGGCTAGGACCACCCTACTACACGC
                                                                                                                                                                                                                         CGATCCCATCTCTGGGAGGCTGCCCAGGTGGTCCCTGATGGACTGGGGCTGGACGAA-CC
                                                                                                                                                                                                                                                                                                                                               G-CACAGCGATCCTCCTGCACCCCTGGCTGCGACA-GACCCGATGCCCCTTAGCCCCAACC 1218
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Sequence 2, Application US/08913050A
Patent No. 5827726
GENERAL INFORMATION:
APPLICANT: NEZU, Jun-ichi
TITLE OF INVENTION: DNA ENCODING PR
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                              RESULT 4
US-08-913-050A-2
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; LOCATION:
US-08-146-421-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
PEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
           ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                       STREET: %1. CITY: Washington
                                                            COUNTRY:
                                                                                                                      ADDRESSEB:
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                                                                                                       3B: BROWDY AND NEIMARK, P.L.L.C. 419 7th Street N.W., Suite 300
                                                            USA
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IBM PC compatible
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Pred. No. 1.4e-99;
D; Mismatches 28
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP PCT
PILING DATE: 15-MAR-1996
ATTORNBY/AGENT INFORMATION:
NAME: YUN, Allen C.
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REFERENCE/DOCKET NUMBER: NE:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA; APPLICATION NUMBER: US/08/913,050A FILING DATE: 05-SEP-1997 PRIOR APPLICATION DATA; APPLICATION NUMBER: JF 57104/1995 FILING DATE: 16-MAR-1995
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Local Similarity 48.1%;
hes 241; Conservative
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ACAGCTGGTTCCGGAAGAAAC
                                ACCCCTGGCTGCGACAGGACC
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                                                                   TGAAAGGGATGCTTGAGTACGAACCGGCCAAGAGGTTCTCCATCCGGCAGATCCGGCAGC
                                                                                                  TTCGCTGCCTCCTTCGTCGGGAGCCAGCTGAACGGCTCACAGCCACAGGCATCCTCCTGC
                                                                                                                                   ACATCGGGAAGGGGAGCTACGCCATCCCGGGCGACTGTGGCCCCCCCGCTCTCTGACCTGC
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Pred. No. 2.6e-09;
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RESULT 5 US-09-016-434-1146

Sequence 1146, Application US/09016434 Patent No. 6500938 GENERAL INFORMATION:

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US-09-016-434-1146
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Best Local Similarity
Matches 241; Conserv
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INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
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NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERRENCE/DOCKET NUMBER: PA
TELECOMMUNICATION INFORMATION:
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CITY: PALO ALTO
STATE: CALIFORNIA
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APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION
TITLE OF INVENTION: PATHMAY GENE EXPRESSION
NUMBER OF SEQUENCES: 1490
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/016,434
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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CLASSIFICATION:
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                                                 ACAACATCACCACGGGTCTGTACCCCTTCGAAGGGGACAACATCTACAAGTTGTTTGAGA
                                                                                                                   ACGGCCTGGACACCTTCTCCGGCTTCAAGGTGGACATCTGGTCGGCTGGGGTCACCCTCT
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Pred. No. 2.6e-09;
0; Mismatches 260
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US-09-996-243-300

Sequence 30 Patent No. GENERAL INE

300, Application US/09996243

APPLICANT:
APPLICANT:
APPLICANT:

Baker, Kevin P. Botstein, David

APPLICANT: Ashkenazi, Avi

INFORMATION:

APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT:

Desnoyers, Luc Eaton, Dan L Ferrara, Napoleone Fong, Sherman

Gerber, Hanspeter Gerritsen, Mary E.

APPLICANT:

Goddard, Audrey Godowski, Paul J. Grimaldi, J. Christopher Gurney, Austin L.

APPLICANT:

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US-09-559-023-1
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APPLICANT: Leal-Pinto, Edgar
APPLICANT: Lipkowitz, Michael
TITLE OF INVENTION: NUCLEIC ACID ENCODING UE
TITLE OF INVENTION: AND METHODS OF USE THEF
FILE REPERENCE: 070165,0574
CURRENT APPLICATION NUMBER: US/09/559,023
CURRENT FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: US 09/221,898
PRIOR FILING DATE: 1998-12-28
                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS:
SOPTWARE: FastSEQ for
SEQ ID NO 1
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                                                                                                                                                                                Matches 117;
                                                                                                                                                                                                Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: US 60/070,215 PRIOR FILING DATE: 1997-12-31
                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: US 60/099,752
PRIOR FILING DATE: 1998-09-10
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                                                         CTCCAGCTGACCCAGAATGTCCACATTACCTTTTCCCCCAATCTTTCCCCAATGCCCCATAAA
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Pred. No. 3.4e-09;
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APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Stewart, Timothy A.
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANTON: Secreted and Transmembra:
TITLE OF INVENTION: NUMBER: U9/09/996,243
CURRENT APPLICATION NUMBER: 60/049787
PRIOR APPLICATION NUMBER: 60/065186
PRIOR APPLICATION NUMBER: 60/065311
PRIOR APPLICATION NUMBER: 60/065311
PRIOR APPLICATION NUMBER: 60/066770
PRIOR APPLICATION NUMBER: 60/066770
PRIOR APPLICATION NUMBER: 60/075945
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PRIOR APPLICATION NUMBER: 60/078910
PRIOR APPLICATION NUMBER: 60/08332
PRIOR PILLING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/08332
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PRIOR APPLICATION NUMBER: 60/084600
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DR FILING DATE: 1998-06-04

PR APPLICATION NUMBER: 60/08028

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PR PILING DATE: 1998-06-05

PR APPLICATION NUMBER: 60/088167

PR PILING DATE: 1998-06-05

PR APPLICATION NUMBER: 60/088202

PR PILING DATE: 1998-06-05

PR PILING DATE: 1998-06-05

PR APPLICATION NUMBER: 60/088212

PR PILING DATE: 1998-06-05

PR APPLICATION NUMBER: 60/088217

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PR APPLICATION NUMBER: 60/088734

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DR FILING DATE: 1998-06-02
DR APPLICATION NUMBER: 60/087827
DR FILING DATE: 1998-06-03
DR APPLICATION NUMBER: 60/088021
DR FILING DATE: 1998-06-04
DR FILING DATE: 1998-06-04
DR APPLICATION NUMBER: 60/088025
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FILING DATE: 1998-05-28
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FILING DATE: 1998-06-02
APPLICATION NUMBER: 60/087609
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PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/08810
PRIOR APPLICATION NUMBER: 60/08810
PRIOR FILING DATE: 1998-06-10
PRIOR PRIOR APPLICATION NUMBER: 60/088824
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088858
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/088861
PRIOR PILING DATE: 1998-06-12
PRIOR APPLICATION NUMBER: 60/0898161
PRIOR PILING DATE: 1998-06-12
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PRIOR PILING DATE: 1998-06-12
PRIOR APPLICATION NUMBER: 60/089514
PRIOR PILING DATE: 1998-06-12
PRIOR APPLICATION NUMBER: 60/089514
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PRIOR APPLICATION NUMBER: 60/08996
PRIOR PILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/09024
PRIOR APPLICATION NUMBER: 60/09025
PRIOR PILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/09035
PRIOR PILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/09044
PRIOR PILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/09045
PRIOR

NUMBER: NUMBER: 60/ : 1998-06-24

60/090557 60/090542

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RESULT 8
US-09-996-243-302
J Sequence 302, Application U.
Patent No. 6478825
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
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Best Local Sim:
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DR APPLICATION NUMBER: 60/09
DR FILING DATE: 1998-07-02
DR APPLICATION NUMBER: 60/09
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FILING DATE: 1998-06-26
APPLICATION NUMBER: 60/
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                     Baker, Kevin P.
Botstein, David
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Pred. No. 8.5e-09;
0; Mismatches 117;
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APPLICANT: Baton, Dan L.
APPLICANT: Perrara, Napoleone
APPLICANT: Perrara, Napoleone
APPLICANT: Penng, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Goddwski, Paul J.
APPLICANT: Godowski, Paul J.
APPLICANT: Giavney, Austin L.
APPLICANT: Hapier, Mary A.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Pan, James
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewarr, Timothy A.
APPLICANT: Stewarr, Timothy A.
APPLICANT: Watanabe, Colin K.
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Daniel
APPLICANT: Chang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Pol
TITLE REFERENCE: P2730P1C13
CURRENT APPLICATION NUMBER: US/09/996,243
CURRENT APPLICATION NUMBER: 00140787
                             PRIOR
OR FILING DATE: 1998-06-04
OR APPLICATION NUMBER: 60/088028
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OR FILING DATE: 1998-06-04
OR APPLICATION NUMBER: 60/088033
OR FILING DATE: 1998-06-04
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OR APPLICATION NUMBER: 60/087607
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OR APPLICATION NUMBER: 60/087609
OR APPLICATION NUMBER: 60/087759
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DR APPLICATION NUMBER: 60/065311
DR APPLICATION NUMBER: 60/066770
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APPLICATION NUMBER: 6
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DR PILING DATE: 1998-06-23

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DR FILING DATE: 1998-06-12
DR APPLICATION NUMBER: 60/089440
DR FILING DATE: 1998-06-16
DR APPLICATION NUMBER: 60/089512
DR APPLICATION NUMBER: 60/089514
DR APPLICATION NUMBER: 60/089514
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DR FILING DATE: 1998-06-09

DR APPLICATION NUMBER: 60/088734

DR FILING DATE: 1998-06-10

DR APPLICATION NUMBER: 60/088738

DR APPLICATION NUMBER: 60/088738

DR FILING DATE: 1998-06-10

DR APPLICATION NUMBER: 60/088742
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APPLICATION NUMBER: 60/089948
FILING DATE: 1998-06-19
APPLICATION NUMBER: 60/089952
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APPLICATION NUMBER:
FILING DATE: 1998-00
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APPLICATION NUMBER: 60/089947
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APPLICATION NUMBER: 60/089532
FILING DATE: 1998-06-17
APPLICATION NUMBER: 60/089538
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FILING DATE: 1998-06-11
APPLICATION NUMBER: 60/088861
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FILING DATE: 1998-06-10
APPLICATION NUMBER: 60/088826
FILING DATE: 1998-06-10
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                              Sequence 2, Application US/08749902
Patent No. 5985635
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Goll, Surya K.
APPLICANT: Hillman, Jennifer L.
TITLE OF INVENTION: NOVEL HUMAN SERINE/THREONINE
TITLE OF INVENTION: PROTEIN KINASES
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Best Local Similarity
Matches 92; Conserv
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CORRESPONDENCE
                NUMBER OF SEQUENCES:
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OR FILING DATE: 1998-06-24
OR APPLICATION NUMBER: 60/090542
OR APPLICATION NUMBER: 60/09057
OR APPLICATION NUMBER: 60/09057
OR APPLICATION NUMBER: 60/090676
OR APPLICATION NUMBER: 60/090676
OR FILING DATE: 1998-06-25
OR APPLICATION NUMBER: 60/090690
OR FILING DATE: 1998-06-25
OR APPLICATION NUMBER: 60/090690
OR FILING DATE: 1998-06-25
OR APPLICATION NUMBER: 60/090694
OR PILING DATE: 1998-06-25
OR APPLICATION NUMBER: 60/090695
OR APPLICATION NUMBER: 60/090696
OR APPLICATION NUMBER: 60/0906966
OR FILING DATE: 1998-06-26
OR APPLICATION NUMBER: 60/090863
OR FILING DATE: 1998-06-26
OR APPLICATION NUMBER: 60/091360
OR FILING DATE: 1998-06-26
OR APPLICATION NUMBER: 60/091360
OR FILING DATE: 1998-07-01
OR APPLICATION NUMBER: 60/091519
OR APPLICATION NUMBER: 60/091519
OR APPLICATION NUMBER: 60/09163
OR FILING DATE: 1998-07-02
OR APPLICATION NUMBER: 60/09163
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APPLICATION NUMBER: 60/090445
FILING DATE: 1998-06-24
APPLICATION NUMBER: 60/090472
FILING DATE: 1998-06-24
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FILING DATE: 1998-06-24
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llarity 85.2%;
Conservative
ADDRESS
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                                                                                                                                                                                                                                                                                                                                                                                                                    Score 82.4; DB 4;
Pred. No. 1.1e-08;
0; Mismatches 16;
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Best Local Similarity
Matches 237, Conserv
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OPERATING SYSTEM: DOS
SOFTWARE: PASCESO Vecrsion 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/749,902
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
APPLICATION NUMBER:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1466 base pair
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NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEPAX: 415-845-4166
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MEDIUM TYPE: Diskett
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CLONE: Consensus
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STRANDEDNESS: sing
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STREET: 3174 Porter Drive
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                                                                                                                                                                                                                                                           TCACCATGCTGGCCGGCCACTACCCCTTCCAGGACTCGGAGCCTGTCCTGCTCTTCGGCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGCGTTTCCCAGTGTGCCAGGCCCACGGGTACTTCTGTCAGCTGATTGACGGCNTGGGGT
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                                   ACCCCTGGCTGCGACAGGACC 1003
                                                                                                                TICGCTGCCTCCTTCGTCGGGAGCCAGCTGAACGGCTCACAGCCACAGGCATCCTCCTGC
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IBM Compatible
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Pred. No. 1.5e-08;
0; Mismatches 264; Indels
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RESULT 11
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CURRENT FILING DATE: 2000-01-24
EARLIER APPLICATION NUMBER: PCT/US99/17130
EARLIER FILING DATE: 1999-07-29
EARLIER APPLICATION NUMBER: 60/094,657
EARLIER APPLICATION NUMBER: 60/095,486
EARLIER APPLICATION NUMBER: 60/095,486
EARLIER FILING DATE: 1998-08-05
EARLIER FILING DATE: 1998-08-05
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EARLIER APPLICATION NUMBER: 60/095,454
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EARLIER APPLICATION NUMBER: 60/095,455
EARLIER PILING DATE: 1998-08-06
NUMBER: DATE: 1998-08-06
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US-09-489-847-38
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LENGTH: 1048
                                                                                                                                   Sequence 245, Application US/09996243 Patent No. 6478825
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                                                                                                                 GENERAL INFORMATION:
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                                                                                                                                 Patent No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                           3.9%;
Local Similarity 87.9%;
nes 87; Conservative
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Ferrara, Napoleone
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Pred. No. 3.2e-08;
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APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Bestein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eston, Dan L.
APPLICANT: Ferrara, Napoleon
APPLICANT: Fong, Sherman APPLICANT:
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FILE REFERENCE: P2730FC13
CURRENT ILLING DATE: 1997-06-16
PRIOR PELLING DATE: 1997-06-16
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PRIOR PELLING DATE: 1997-11-12
PRIOR PELLING DATE: 1997-11-13
PRIOR PELLING DATE: 1997-11-34
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PRIOR PELLING DATE: 1999-10-36
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PRIOR PELLING DATE: 1999-10-36
PRIOR PELLING DATE: 1999-0-76
PRIOR
          OR APPLICATION NUMBER: 60/088742
OR PILING DATE: 1998-06-10
OR APPLICATION NUMBER: 60/08810
OR PILING DATE: 1998-06-10
OR APPLICATION NUMBER: 60/088824
OR APPLICATION NUMBER: 60/088826
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OR APPLICATION NUMBER: 60/090445
OR FILING DATE: 1998-06-24
OR APPLICATION NUMBER: 60/090472
OR FILING DATE: 1998-06-24
OR APPLICATION NUMBER: 60/090535
OR APPLICATION NUMBER: 60/090540
OR APPLICATION NUMBER: 60/090540
OR FILING DATE: 1998-06-24
OR APPLICATION NUMBER: 60/090542
OR APPLICATION NUMBER: 60/090542
OR APPLICATION NUMBER: 60/09057
OR FILING DATE: 1998-06-24
OR PILING DATE: 1998-06-25
OR FILING DATE: 1998-06-25
OR APPLICATION NUMBER: 60/090676
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OR APPLICATION NUMBER: 60/089653
OR PILING DATE: 1998-06-18
OR APPLICATION NUMBER: 60/089801
OR PILING DATE: 1998-06-18
OR APPLICATION NUMBER: 60/089907
OR FILING DATE: 1998-06-18
OR APPLICATION NUMBER: 60/089908
OR APPLICATION NUMBER: 60/089947
OR PILING DATE: 1998-06-19
OR APPLICATION NUMBER: 60/089947
OR PILING DATE: 1998-06-19
OR APPLICATION NUMBER: 60/089952
OR APPLICATION NUMBER: 60/090246
OR PILING DATE: 1998-06-29
OR APPLICATION NUMBER: 60/090252
OR FILING DATE: 1998-06-22
OR APPLICATION NUMBER: 60/090254
OR APPLICATION NUMBER: 60/090355
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PR FILING DATE: 1998-06-17

R APPLICATION NUMBER

R PILING TO
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APPLICATION NUMBER: 60/
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APPLICATION NUMBER: 60/0
FILING DATE: 1998-06-17
APPLICATION NUMBER: 60/0
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APPLICATION N
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APPLICATION N
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FILING DATE: 1998-06-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER: 60/090444
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: 1998-06-17
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1998-06-17
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RESULT 12
US-08-157-101A-
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GENERAL INFORMATION:
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Best Local Similarity 72.5%;

Matches 103; Conservative
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COMPUTER READABLE FORM:
MEDLUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PACENTIN Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/157,101A
                                                                                                                                                         NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSE: PILLSBURY, MADISON & SUTRO
STREET: 1100 NEW YORK AVENUE, N.W.
CITY: WASHINGTON
                                                                                                                                                                                                                                                                         APPLICANT: KURIHARA, TATSUYA
APPLICANT: MATSUKURA, SHIGEKAZU
APPLICANT: TSURUOKA, NOBUO
APPLICANT: ARIMA, KENJI
APPLICANT: NISHIHARA, TATSURO
                                                                                                                                                                                                                                          TITLE OF INVENTION: ANTI-HB8 ANTIBODY GENES TITLE OF INVENTION: PLASMIDS THEREFOR
                                                                                                            COUNTRY: U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 60/091982
FILING DATE: 1998-07-07
APPLICATION NUMBER: 60/092182
FILING DATE: 1998-07-09
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FILING DATE: 1998-07-01
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FILING DATE: 1998-06-26
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FILING DATE: 1998-07-02
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FILING DATE: 1998-07-02
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FILING DATE: 1998-07-02
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FILING DATE: 1998-07-02
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FILING DATE: 1998-06-26
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FILING DATE: 1998-06-25
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Pred. No. 2.7e-08;
0; Mismatches 39;
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APPLICANT: Lebby, K.
APPLICANT: MCKay, C.
APPLICANT: BOSBONE, S.
APPLICANT: BOSBONE, S.
APPLICANT: BOSBONE, S.
TITLB OF INVENTION: SECRETED PROTEINS AND USES THE PILE REPERENCE: 7853-144
CURRENT APPLICATION NUMBER: US/09/336,536
CURRENT FILING DATE: 1999-06-18
NUMBER OF SEQ ID NOS: 75
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 66
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US-09-336-536-66
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                                                                                                       Query Match
Best Local Similarity 89:
Matches 85; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 66, Application US/09336536 Patent No. 6406884
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Best Local
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INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 1066 base pairs
                                                                                                                                                                                                                     LENGTH: 1927
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                      NAME/KBY: modified_base
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NAME: TITUS, MARLANA K
REGISTRATION UNMBER: 35843
REFERENCE/DOCKET NUMBER: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION: TELEPHONE: 202-861-3711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
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1826
                                                                               1965
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                       2025 АЛЛАЛАЛЛАЛАЛЛАЛАЛЛАЛЛАЛЛАЛЛАЛЛАЛАЛ 2059
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                                                                                                                     3.9%;
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                                                                                                        Score 79.6; DB 4;
Pred. No. 4.3e-08;
0; Mismatches 10
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Pred. No. 3.
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                                                                                                                                  DB 4;
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                                                                                                                                 Length 1927;
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NUMBER OF SEQ ID NOS: 18
SOFTWARE: Microsoft Office 97
SEQ ID NO 1
LENGTH: 1882
TYPE: DNA
ORGANISM: Hordeum vulgare
US-09-370-253-1
                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:

APPLICANT: Allen, Stephen M.

APPLICANT: Sakai, Hajime

APPLICANT: Thorpe, Catherine J.

TITLE OF INVENTION: Amino Acid Transporters

FILE REFERENCE: BB-1200

CURRENT APPLICATION NUMBER: US/09/370,253

CURRENT PILING DATE: 1999-08-09

EARLIER APPLICATION NUMBER: 60/097,222

EARLIER APPLICATION NUMBER: 00/097,222

EARLIER PILING DATE: August 20, 1998
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US-09-370-253-1
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Patent No. 6501008
GENERAL INFORMATION:
APPLICANT: Nevine, Donald J.
APPLICANT: Simmons, Carl
APPLICANT: The Regents of the University of California
                                                                 Query Match 3.8%; Score 79.2; DB 3; Length 1882; Best Local Similarity 83.3%; Pred. No. 5.2e-08; Matches 90; Conservative 0; Mismatches 18; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/09370253 Patent No. 6165792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match 3.8%; Score 79.2; DB 4; Best Local Similarity 75.0%; Pred. No. 4.4e-08; Matches 99; Conservative 0; Mismatches 33;
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SEQ ID NO 1
LENGTH: 1091
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CURRENT APPLICATION NUMBER: US/09/328,965
CURRENT FILING DATE: 1999-06-06
EARLIER APPLICATION NUMBER: US 60/088,780
EARLIER FILING DATE: 1998-06-10
NUMBER OF SEQ ID NOS: 3
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LOCATION: (68)..(979)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE: OTHER INFORMATION: maize coleoptile endo-1,3;1,4-beta glucanase cDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: endo-1,3;1,4-beta glucanase
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Search completed: January 16, 2004, 16:49:41 Job time: 135.44 Becs

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RESULT 2 US-10-098-841-271 ; Sequence 271, Application US/10098841 ; Publication No. US20020197679A1 ; GRIERAL INFORMATION: ; APPLICANT: Tang, Y. Tom ; APPLICANT: Tand, Vinod ; APPLICANT: Xu, Chenghua ; APPLICANT: Xu, Chongjun ; APPLICANT: Xu, Chongjun ; APPLICANT: Xu, Chongjun ; APPLICANT: Ma, Yunqing	9y 1201 ANCTORACCOMACCITECAGACGACAMAGCACACAMAGCACAMAGCACAMAGCACAMAGCACAMAGCACAMAGCACAMAGCACAMAGCACAMAGCACAMAGCACAMAGCACAMAGCACAMAGCACAMAGCACAMAGCACAMAGCACAMAGCACAMAGCACACAMAGCACAMAGCACAMAGCACAMAGCACAMAGCACAMAGCACAMAGCACAMAGCACAMAGCACAMAGCACAMAGCACAMAGCACAMAGCACAMAGCACAMAGCACAMAGCACAMAGCACAMAGCACACAMAGCACACAMAGCACACAMAGCACACAMAGCACACAMAGCACACAMAGCACACAMAGCACACAMAGCACACACA	

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Oy 1561 CCTTTCAGAGAAAGGGAGGTATCCCTGTGCCAAAGGCCTCCAGGCCTCCCCTGCAACT 1620 Db 1651 CCTTTTCAGAGAAAGGGAGGTATCCCTGTGCCAAAGGCTCCAGGCCTCTCCCCTGCAACT 1710 Oy 1621 CAGGACCCAAGCCCAGCTCACTCTGGGGAACTGTGTTCCCAGGCTTCTTGATT 1680	1501		1381	1321 GTGCCAAGCCCTGTTCTCGGTGCTGGGAGTAAGGAAGGAA	1261 TGCTGTGTACACATCTGCTTTGTTCCACACACATGCAGTTCCTGCTTGGGTGCTTATCAG	1201 AACTGAGCCAAACCTTCAGGAGGAGGAAAGGCAGAAGCCTGTGTGGAGTG	1141 CGCTCAGCTGCCAACAGTGGATTGAGTTTGGGGGTAGCTCCAAGCCTTCTCCTGCCTCTG 1131 CGCTCAGCTGCCAACAGTGGATTTGGGGGGTAGCTCCAAGCCTTCTCCTGCCTCTG 1231 CGCTCAGCTGCCAACAGTGGATTTGGGGGTAGCTCCAAGCCTTCTCCTGCCTCTG	1081 GCCAGGGAAGAGGACGACGACAAGTGGTTCTGTATGGCTAGGACCACCCTACTACACACAC		961	Oy 901 TCGGCCCCTGCCCGCTGTCTGGTTCGCTGCCTCCTTCGTCG	Qy 841 GAGCCTGTCCTGCTCTTCGGCAAGATCCGCCGGGGGCCTACGCCTTGCCTGCAGGCCTC 900	Oy 781 TGGAGCCTGGGCGTGGCGCTCTTCACCATGCTGGCCGGCC	Qy 721 TACGTGGGACCTGAGATACTCAGCTCACGGGCCTCATACTCGGGCAAGGCAGCCGATGTC 780	Qy 661 GACTCCTGCGTGCTGACTGGGCCAGATGATTCCCTGTGGGACAAGCACGCGTGCCCAGCC 720	Qy 601 CTGTGTCGCTTTGTCTTCGCTGAGAGGAAGAAGAAGCTGGTGCTGGAGAACCTGGAG 660	Db 631 CAGATGGCCACCGCCCTGGCGCACTGTCACCAGCACGGTCTGGTCCTGCGTGATCTCAAG 690

RESULT 3 US-09-35-101-56 US-09-35-101-56 US-09-35-101-56 US-09-35-101-56 Sequence 260, Application US/09925301 Sequence 260, Application US/09925301 Sequence 260, Application US/09925301 Patent No. US2003052308A1 GENERAL IMPORMATION: Anciet Acids, Proteins and Antibodies FITTLS OF INVESTICATION	Db 1711 CAGGACCCAAGCCCAGCTCACTCTGGGAACTGTGTTCCCAGCATCTCTGATT 1770 1681 AAGAGATTCTCCTTCCAGGCCTAAGCCTGGGATTTGGGCCAGAGATAAGAATCCAAACTA 1740
94 GAGAACCTGGGGGCTTGCCTGGCCCAGATGATTCCCTGTGGGACAGACCA 708	Db 305

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SOPTWARE: PASTSEQ for Windows Version
SEQ ID NO 7
LENGTH: 2389
TYPE: DNA
ORGANISM: Homo sapiens
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Patent No. US20020034780A1
GENERAL INFORMATION:
                                                                                                                                                 Query Match 99.7%;
Best Local Similarity 99.9%;
                                                                                                                                Matches 2053;
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FILE REPERINCE: 35800/20996
CURRENT APPLICATION NUMBER: US/09/799,875
CURRENT FILING DATE: 2001-03-06
CURRENT FILING DATE: 2001-03-06
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APPLICANT: Kapeller-Libermann, Rosana
APPLICANT: Williamson, Mark
                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: 60/182,059
PRIOR PILING DATE: 2000-02-11
PRIOR APPLICATION NUMBER: 09/659,287
PRIOR PILING DATE: 2000-09-12
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61 CCTCTGGCTGCTGCGGGTTCCCTGTCCAGGAAGAAGCGGTTGGAAGTTGGATGACAAC 120
                                                                            Conservative
                                                                                                                                0; Mismatches
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RESULT 2 US-10-098-841-271 ; Sequence 271, Application US/10098841 ; Publication No. US20020197679A1 ; GENRRAL INFORMATION: ; APPLICANT: Tang, Y. Tom ; APPLICANT: Liu, Chenghua ; APPLICANT: Asundi, Vinod ; APPLICANT: Xu, Chongjun ; APPLICANT: Zhou, Ping ; APPLICANT: Zhou, Ping ; APPLICANT: Ma, Yunqing		1861 GGCCACCTGGAAAGTCCCAGGTGGGACTCTTCTGGGGACACTTGGGGTCCACAATCCCAG	1741 TGAGGCTACTTCTTGTCTAACTCAAGACTGTTCTGGAATGAGGGTCCAGGCCTTCTCAACC		OY 1381 TGCTCACAGAGATGACAAACTGGCATCCTTGAGCTGACAACACTTTTCCATGACCATAGG 1440		OY 1201 AACTGAGCCAAACCTTCAGTGCCTTCCAGAAGGGAAAAGGCAGAAGCCTGTGTGTG

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APPLICANT: Wang, Jian-Rui
APPLICANT: Zhao, Qing A.
APPLICANT: Ren, Feiyan
APPLICANT: Wang, Dunrui
APPLICANT: Wang, Zhiwei
APPLICANT: Wang, Zhiwei
APPLICANT: Wang, Zhiwei
APPLICANT: Zhang, Jie
APPLICANT: Drmanac, Radoje T.
CURRENT APPLICATION INDER: US/10/098,841
CURRENT APPLICATION NUMBER: US/10/098,841
CURRENT APPLICATION NUMBER: 09/598,042
PRIOR APPLICATION NUMBER: 09/592,317
PRIOR APPLICATION NUMBER: 09/552,317
PRIOR APPLICATION NUMBER: 09/552,317
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 331
SOFTWARE: Dr PLGenes Version 1.0
SEQ ID NO 271
LENGTH: 2092
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
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229 GCTGTGGCCACTGCCTCCCGTCTTGGGCCCTATGTCCTCCTGGAGCCCGAGGAGGGCGGG	169 CCCAGACTGCCCCTGCCTGTTGCCCCTGAGCCCACCTACTGCTCCAGATCGTGCAACT	Oy 109 TTGGATGACAACTTAGATACCGAGGGTCCCGGTCCAGAAACGAGCTCGAAGTGGGCCCCAG 168	Gy 49 ATGCGAGCCACCCTCTGGCTGCTGCTGCGGGTTCCCTGTCCAGGAAGAAGCGGTTGGAG 108	Query Match 85.9%; Score 1767.8; DB 9; Length 2048; Best Local Similarity 95.9%; Pred. No. 0; Matches 1882; Conservative 4; Mismatches 1; Indels 76; Gaps 4;	NAME/KEY: misc_feature; ; LOCATION: (67) ; OTHER INFORMATION: n equals a,t,g, or c US-09-925-301-260	; PEATURE: ; NAME/KEY: misc_feature ; LOCATION: (66)	SEQ ID NO 260 LENGTH: 2048 TYPE: DNA TYPE: DNA ORGANISM: Homo sapiens	PRIOR APPLICATION NUMBER: 60/124,270 PRIOR FILING DATE: 1999-03-12 NUMBER OF SEQ ID NOS: 1694 SOFTWARE: PATENTIN Ver. 2.0	CURRENT APPLICATION NUMBER: US/09/925,301 ; CURRENT FILING DATE: 2001-08-10 ; PRIOR APPLICATION NUMBER: PCT/US00/05862 ; PRIOR FILING DATE: 2000-03-08	GENERAL INFORMATION: APPLICANT: Rosen et al. TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies FILE REFERENCE: PAIO6	RESULT 3 US-09-925-301-260 ; Sequence 260, Application US/09925301 ; Patent No. US20020052308A1	Db 2071 GAATTATGAAATAAAAAAAAA 2092	2011 GTCCATACTCTAGGTTTTGGATACCATGAGTATGTTTTACCTGTGCCTAATAAAGGA	1951 GTCCATACTCTAGGTTTTTGGATACCATGAGTATGTTTTTAGGTTCTCTGGGAATACCTAATAAAGGA	1861 GGCCACCTCGAAAGTCCCAGGTTGAGGGACAGGTTAGGGGGGTCTGTCCTGTGTGGGGACAGGGTTTAGGCAGGGTCTGTCCTGTGTGTG	TGAGGCTAGTTCTTGACCTGAAGACTGTTCTGAAGACTGTTCTGAAGACTTAGGCAGACCTGTCAACC	1771 AAGAGATTCTCCTTCCAGGCCTAAGCAGGGATTTGGGCCAGAGATAAGAATCCAAACTA	Db 1711 CAGGACCCAAGCCCAGCTCACTCTGGGAACTGTGTTCCCAGCATCTCTGTCCTCTTGATT 1770 OV 1681 AAGAGATTCTCCTTCCAGGCCTAAGCCTGGGATTTGGGCCAGAGATAAGAATCCAAACTA 1740
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Sequence 9, Application US/09799875

Patent No. US20020034780A1

JENERAL INFORMATION:
APPLICANT: Meyers, Rachel
APPLICANT: Williamson, Mark
TITLE OF INVENTION: No. US20020034780A1el Human Pro
TITLE OF INVENTION: NUMBER: US/09/799,875

CURRENT APPLICATION NUMBER: US/09/799,875

CURRENT APPLICATION NUMBER: 60/182,059

PRIOR APPLICATION NUMBER: 09/659,287

PRIOR APPLICAT
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           52.0%;
           Score 1070.8;
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         Length 1074;
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                                                                       CCCTTAGCCCCAACCCGATCCCATCTCTGGGAGGCTGCCCAGGTGGTCCCTGATGGACTG 1068
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540 588 480 528 420 468

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1008 960

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WS-10-024-828-3

US-10-024-828-3

Sequence 3, Application US/10024828

Publication No. US20030036051A1

REPLICANT: LIFORMATION:

APPLICANT: Wirca, Duke
APPLICANT: Hid, Timothy A.
APPLICANT: Marken, John S.

TITLE OF INVENTION: Human cDNAs Encoding Polypeptides Having Kinase
TITLE OF INVENTION: Punctions
FILE REFERENCE: 2877-US
CURRENT APPLICATION NUMBER: US/10/024,828
CURRENT PILING DATE: 2001-12-18
PRIOR APPLICATION NUMBER: US/09/509,902A
PRIOR FILING DATE: 199-08-03

ROTWARE: OF SEQ ID NOS: 16
SOFTWARE: PATENT FOR SEQ ID NOS: 16
SOFTWARE: PATENT PILING DATE: 199-08-03

LENGTH: 1085
TYPE: DNA
CRGANISM: Homo sapiens
US-10-024-828-3
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                                                                     CAGATGGCCACCGCCCTGGCGCACTGTCACCAGCACGGTCTGGTCCTGCGTGATCTCAAG
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GENERAL INFORMATION:

APPLICANT: Pyle, Ruth
APPLICANT: XL, Jiangchun
APPLICANT: Secrist, Heather
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIACNOSIS OF COLON CANCER
FILE REFERENCE: 210121.552
CURRENT APPLICATION NUMBER: US/09/919,580
CURRENT APPLICATION NUMBER: US/09/919,580
CURRENT FILING DATE: 2001-07-30
NUMBER OF SEQ ID NOS: 934
SOPTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 580
LENGTH: 541
TYPE: DNA
ORGANISM: Homo Bapiens
US-09-919-580-580
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Best Local Similarity 99.1%;
Matches 536; Conservative
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GACAATATTCCCTGCTCACAGAGATGACAAACTGGCATCCTTGAGCTGACAACACTTTTC 1426
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                                             GGTGCTTATCAGGTGCCAAGCCCTGTTCTCGGTGCTGGGAGTACAGCAGTGAGCAAAGGA 1366
                                                                                                            ACAGCCACAGGCATCCTCCTGCACCCCTGGCTGCGACAGGACCCGA 1006
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                                                                                         ACAGCCACAGGCATCCTCCTGCACCCCTGGCTGCGACAGGACCCGA 1085
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Pred. No. 1.9e-105;
0; Mismatches 5;
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APPLICANT: Aglate, Paul A.

APPLICANT: Aglate, Robert

APPLICANT: Harlocker, Susan L.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER

FILE REFERENCE: 210121.497

CURRENT APPLICATION NUMBER: US/09/867,701

CURRENT APPLICATION NUMBER: US/09/867,701

CURRENT FILING DATE: 2001-05-29

NUMBER OF SEQ ID NOS: 10912

SOFTWARE: Fast-SEQ for Windows Version 4.0

SEQ ID.NO 10282

LENGTH: 426

TYPE: DNA

ORGANISM: Homo sapien
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US-09-867-701-10282/c
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Patent No. US20020132237A1
GENERAL INFORMATION:
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Best Local
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20.7%; Score 426; DB 10;
Local Similarity 100.0%; Pred. No. 2.3e-82;
hes 426; Conservative 0; Mismatches 0;
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                                                                                                                                                                                              CTTCTGACCTGAGCACCAAGGTTGAGGGACAGGATTAGGCAGGGTCTGTCCTGTGGCCAC 127
                                                                                                                                                                                                                                                                                                          TAGTTCTTGTCTAACTCAAGACTGTTCTGGAATGAGGGTCCAGGCCTGTCAACCATGGGG 1800
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                                                                                                            CTGGAAAGTCCCAGGTGGGACTCTTCTGGGGACACTTGGGGTCCACAATCCCAGGTCCAT 67
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APPLICANT: Jones, Lee William
APPLICANT: Stache-Crain, Birgit
TITLE OP INVENTION: Human Genes and Gene Products
FILE REFERENCE: 1624.002
CURRENT APPLICATION NUMBER: US/09/803,719
CURRENT APPLICATION NUMBER: 60/188,609
PRIOR APPLICATION NUMBER: 60/188,609
PRIOR APPLICATION NUMBER: 60/180,609
PRIOR APPLICATION NUMBER: 50/180,609
PRIOR PILING DATE: 2000-03-09
NUMBER OF SEG ID NOS: 2396
SOFTWARE: PASTSEQ for Windows Version 4.0
SEO ID NO 519
LENGTH: 396
TYPE: DNA
ORGANISM: Homo sapiens
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APPLICANT: Rescobedo, Jaime
APPLICANT: Rescobedo, Jaime
APPLICANT: Innis, Michael A.
APPLICANT: Garcia, Pablo Domin
APPLICANT: Sudduth-Klinger, Ju
APPLICANT: Reinhard, Christoph
APPLICANT: Reinhard, Gilipo
APPLICANT: Rennedy, Gillia C.
APPLICANT: Pot, David
APPLICANT: Pot, David
APPLICANT: Lamson, George
APPLICANT: Lamson, George
APPLICANT: Crkvenjakov, Radomi
APPLICANT: Dickson, Mark
APPLICANT: Dickson, Mark
APPLICANT: Leshkowitz, Dena
APPLICANT: Garcia, Veronica
APPLICANT: Jones, Lee William
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Publication No. US20030044783A1
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GCCCTGCACTGCCCTACAGGCACTTGAGATACCTGCAAGGTGT
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Crkvenjakov, Radomir
Dickson, Mark
Drmanac, Snezana
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Kennedy, Giulia C.
Pot, David
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APPLICANT: Young, Faul
APPLICANT: Soppet, Daniel
APPLICANT: Soppet, Daniel
APPLICANT: Bondress, Gregory
APPLICANT: Buncr, Meena
APPLICANT: Buncr, Reinhard
APPLICANT: Carter, Kenneth
TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using
TITLE OF INVENTION: Signature Gene Sets
FILE REFERENCE: 689290-64
CURRENT APPLICATION NUMBER: US/09/873,367C
CURRENT APPLICATION NUMBER: U.S. 60/236,891
PRIOR APPLICATION NUMBER: U.S. 60/236,891
PRIOR APPLICATION NUMBER: U.S. 60/236,842
PRIOR APPLICATION NUMBER: U.S. 60/244,867
PRIOR FILING DATE: 2000-09-29
PRIOR APPLICATION NUMBER: U.S. 60/244,867
PRIOR FILING DATE: 2000-11-01
NUMBER OF SEQ ID NOS: 1067
SOPTWARE: Patentin version 3.0
SEQ ID NO 341
LENGTH: 353
TYDE: NNA
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US-09-873-367C-341/c
. Sequence 341, Application US/09873367C
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US-09-925-301-525
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ORGANISM: Homo sapiens
US-09-873-367C-341
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                                                                                                        Sequence 525, Application US/09925301
Patent No. US20020052308A1
GENERAL INFORMATION:
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Best Local Similarity 95.2%;
Matches 336; Conservative
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA106
CURRENT APPLICATION NUMBER: US/09/925,301
CURRENT FILING DATE: 2001-08-10
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Pred. No. 1.7e-58;
0; Mismatches 16;
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PRIOR APPLICATION NUMBER: 09/693,267
PRIOR PILING DATE: 2000-10-20
PRIOR PILING DATE: 2000-09-19
PRIOR PILING DATE: 2000-09-19
PRIOR PILING DATE: 2000-09-19
PRIOR PILING DATE: 2000-09-19
PRIOR APPLICATION NUMBER: 09/616,847
PRIOR APPLICATION NUMBER: 09/596,193
PRIOR PILING DATE: 2000-06-17
PRIOR APPLICATION NUMBER: 09/574,454
PRIOR PILING DATE: 2000-05-19
PRIOR APPLICATION NUMBER: 09/574,954
PRIOR PILING DATE: 2000-05-19
PRIOR APPLICATION NUMBER: 09/519,705
PRIOR PILING DATE: 2000-03-07
INUMBER OF SEQ ID NOS: 752
SEQ ID NO 116
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PRIOR FILING DATE: 2000-03-08
PRIOR PILING DATE: 1009-03-12
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1694
SOPTWARE: PATENTIN Ver. 2.0
SEQ ID NO 525
LENGTH: 562
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NAME/KEY: misc feature

LOCATION: (515)

OTHER INFORMATION: n equals a,t,g, or

NAME/KEY: misc feature

LOCATION: (526)

OTHER INFORMATION: n equals a,t,g, or

NAME/KEY: misc_feature

LOCATION: (557)

COURDE TAYONALATION: n equals a,t,g, or

NAME/KEY: misc_feature
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Best Local
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TITLE OF INVENTION: NO. US20030228584A1e1
FILE REFERENCE: 21272-045
CURRENT APPLICATION NUMBER: US/10/291,172
CURRENT FILING DATE: 2000-11-08
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ORGANISM: Homo sapiens
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LENGTH: 1909
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96.7%;
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Pred. No. 2.5e-48;
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RESULT 12
US-10-119-926-73
US-10-119-926-73
Sequence 73, Application US/10119926
Publication No. US20030104413A1
GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: ABundi, Vinod
APPLICANT: Ren, Feiyan
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; PEATURE:
; NAME/KEY: CDS
; LOCATION: (135)..(!
US-10-291-172-116
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Best Local S
Matches 447
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Local Similarity 60.7%;
1e8 447; Conservative
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Pred. No. 6.8e-47;
0; Mismatches 288;
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APPLICANT: Chen, Rui-hong
APPLICANT: Wehrman, Tom
APPLICANT: Xhou, Ping
APPLICANT: Xu, Chongjun
APPLICANT: Yang, Yonghong
APPLICANT: Yang, Yonghong
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. US20030104413A1el Nucleic Aci
TITLE OF INVENTION: No. US20030104413A1el Nucleic Aci
TITLE OF INVENTION: NO. Polyperides
FILE REFERENCE: 789CIP2BCON
CURRENT APPLICATION NUMBER: US/10/119,926
CURRENT FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 09/574,454
PRIOR APPLICATION NUMBER: 09/519,705
PRIOR APPLICATION NUMBER: 09/519,705
PRIOR FILING DATE: 2000-03-07
NUMBER OF SEQ ID NOS: 108
SOFTWARE: pt FL_genes Version 1.0
SEQ ID NO 73
LENGTH: 1909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; LENGTH: 1909
; TYPE: DNA
; ORGANISM: Homo sapi
; FRATURE:
; NAME/KEY: CDS
; LOCATION: (135)...(9
US-10-119-926-73
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447; Conserv
                                            CGCTCTTCACCATGCTGGCCGGCCACTACCCCCTTCCAGGACTCGGAGCCTGTCCTGCTCT
                                                                                   TCCTCAACACCACTGGGACCTACTCCGGAAAGGCTGCGGACGTTTGGAGCCTGGGGGTGA
                                                                                                     TACTCAGCTCACGGGCCTCATACTCGGGCAAGGCAGCCGATGTCTGGAGCCTGGGCGTGG
                                                                                                                                            AGGGGGAAGATGATGCTTTGTCAGACAAACATGGCTGCCCAGCCTACGTGAGCCCTGAGA
                                                                                                                                                              CTGGGCCAGATGATTCCCTGTGGGACAAGCACGCGTGCCCAGCCTACGTGGGACCTGAGA
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 TCGGCAAGATCCGCCGCGGGGCCTACGCCTTGCCTGCAGGCCTCTCGGCCCCTGCCCGCT
                             TGCTCTACACCCTTCTGGTTGGACGATACCCCTTCCATGACTCAGACCCCAGTGCCCTTT
                                                                                                                                                                                                                                                                                                                                                                          AMACCAAGGCCTATGTCTTTTGAGAAGGACTTTGGGGACATGCACTCCTATGTGCGAA
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Pred. No. 6.8e-47;
0; Mismatches 288;
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1998

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APPLICANT: Sues Stuart
APPLICANT: Jed G. Nuchtern
APPLICANT: Jed G. Nuchtern
APPLICANT: Jason M. Shohet
TITLE OF INVENTION: GENES REGULATED BY MYCN ACT
FILE REFERENCE: PA-0046 US
CURRENT APPLICATION UNMBER: US/10/084,817
CURRENT FILING DATE: 2002-02-25
PRIOR APPLICATION NUMBER: 60/270,784
PRIOR APPLICATION NUMBER: 60/270,784
PRIOR APPLICATION NUMBER: 60/270,784
PRIOR APPLICATION NUMBER: 60/270,784
PRIOR APPLICATION NUMBER: 501-02-23
NUMBER OF SEQ ID NOS: 365
SOPTWARE: PERL Program
SEQ ID NO 300
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; PARTURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte
US-10-084-817-300
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US-10-084-817-300
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Best Local Similarity
Matches 484; Conserv
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TYPE: DNA
         1879
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                                                                                                                                                CACCTGCAAGAAGCTGAGAGAAGGAGGCAGCCAGACTGTTCTACCAGATTGCCTCGGC
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         CTTTAAGGACGAAGAGAGGACTCGGGTCAAGCTGGAAAGCCCTGGAAGACGCCTACATTCT
                                      CTTCGCTGACCGTGAGAGGAAGAAGCTGGTGGTGGAGAACCTGGAGGACTCCTGCGTGCT
                                                                                                                                                                                  AAGCCGCCACCGTATCCCTGAGCCTGAGGCTGCCGTGCTCTTCCGCCAGATGGCCACCGC
                                                                                                                                                                                                                     TGAGACCAAAGCCTATGTGTTCTTTGAGCGAAGCTATGGGGACATGCATTCCTTCGTCCG
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p. US20030119009A1
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Pred. No. 1.5e
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Best Local Simi
Matches 483;
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TITLE OF INVENTION: GENES DIFFERENTIALLY EXPRESSED IN VASCULAR TISSUE ACTIVATION
FILE REFERENCE: PA-0028 US
CURRENT APPLICATION NUMBER: US/10/044,090
CURRENT FILING DATE: 2002-01-09
NUMBER OF SEQ ID NOS: 850
SOFTWARE: PERL Program
SEQ ID NO 269
LENGTH: 3280
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAMB/KEY: misc feature
OTHER INFORMATION: Incyte ID No. US20020137081A1 1820904CB1
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CAGCGGAGAGGAGCTGGTGTGCAAGGTGTTTGATATCAGCTGCTACCAGGAATCCCTGGC
                                                                                                                                                             TACAGGCACTGAGTATACCTGCAAGGTGTACCCCGTCCAGGAAGCCCTGGCCGTGCTGGA 374
                                                                                                                                                                                                 GAAATACTTATTGTTGGAACCTCTGGAGGGAGACCACGTTTTTCGTGCCGTGCATCTGCA
                                                                                                                                                                                                                            GCCTATGTCCTCTGGAGCCCGAGGAGGGCGGGCGGGCCTACCGGGCCCTGCACTGCCC
                                                                                                                                                                                                                                                                     CCTCGGCTCCCCGAGCCCCGAGACTCCGAACTTGTCGCATTGCGTTTCTTGTATCGG
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                                                     ACCGTGCTTTTGCCTGTCTGCTCATAGTAACATCAACCAAATCACTGAAATTATCCTGGG
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                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                         12.2%;
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                                                                                                                                                                                                                                                                                                                                                           Score 251.4; DB 14; Length 3280; Pred. No. 3e-44;
                                                                                                                                                                                                                                                                                                                                          Mismatches 386;
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APPLICANT: SEILHAMER, Jeffrey J.
APPLICANT: PORTER, Gordon J.
APPLICANT: MIKITA, Thomas
APPLICANT: TAI, Julie
TITLE OF INVENTION: GENES EXPRESSED IN FOAM CELL DIE
FILE REFERENCE: PA-0025 PCT
CURRENT APPLICATION NUMBER: US/10/240,965
CURRENT FILING DATE: 2002-10-04
PRIOR APPLICATION NUMBER: 60/195,106
PRIOR APPLICATION NUMBER: 60/195,106
PRIOR FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 276
SOFTWARE: PERL PROGRAM
SEQ ID NO 168
LENGTH: 3324
TYPE: DNA
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US-10-240-965-168
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Publication No. US20030165924A1
GENERAL INFORMATION:
APPLICANT: INCYTE GENOMICS, INC.
APPLICANT: SHIFFMAN, DOV
APPLICANT: SHIFFMAN, DOV
APPLICANT: SONGYI, ROland
APPLICANT: LAWN, Richard M.
                 ORGANISM: Homo sapiens
PEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incyt
PEATURE:
NAMB/KBY: unsure
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; OTHER INFORMATION:
US-10-240-965-168
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Best Local Similarity
Matches 400; Conserva
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Pred. No. 2.7e-43;
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Search completed: January 16, 2004, 20:19:03 Job time: 717.201 secs

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Title:
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| cgn2_6/ptodata/1/1aa/5A_COMB.pep:*
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      GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
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    US-09-328-352-5099
US-09-384-162-16
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US-09-252-991A-24993
US-09-482-273-211
US-08-469-537A-35
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US-08-444-083-8
US-08-444-745-8
US-08-443-129-8
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US-08-98-819-11
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(without alignments)
721.299 Million cell updates/sec
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Sequence 9, Appli
Sequence 25990, A
Sequence 18605, A
Sequence 31777, A
Sequence 2095, Ap
Sequence 2095, Ap
Sequence 11,17, Ap
Sequence 17117, Ap
Sequence 211, Appl
Sequence 21, Appl
Sequence 36, Appl
Sequence 36, Appl
Sequence 8, Appli
Sequence 11, Appli
Sequence 13, Appli
Sequence 14, Appli
Sequence 14, Appli
Sequence 15, Appli
Sequence 16, Appli
Sequence 17, Appli
Sequence 18, Appli
Sequence 19, Appli
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29 7 2.0 232 4 30 7 2.0 295 31 7 2.0 286 4 33 7 2.0 346 3 34 7 2.0 346 3 35 7 2.0 346 3 36 7 2.0 380 4 38 7 2.0 380 4 38 7 2.0 380 4 38 7 2.0 380 4 38 7 2.0 380 4 39 7 2.0 380 4 39 7 2.0 380 4 39 7 2.0 380 4 41 7 2.0 383 3 41 7 2.0 419 4 44 7 2.0 419 4 44 7 2.0 419 4 45 7 2.0 419 4 45 7 2.0 419 4 45 7 2.0 419 4 45 7 2.0 419 4 45 7 2.0 419 4 45 7 2.0 419 4 46 7 2.0 393 3 41 7 2.0 419 4 47 2.0 419 4 48 7 2.0 419 4 49 7 2.0 419 4 49 7 2.0 419 4 40 7 2.0 393 3 40 7 2.0 419 4 41 9 2.0 10 NOS DEQUARRED TO THOCHY A. APPLICANT: Marken, John S. TITLE OF INVENTION. NUMBER: U. CURRENT FILLING DATE: 199-08 40 10 NO 9 41

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FILE REPERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 25890
LENGTH: 731
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-25890
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US-09-252-991A-18605
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US-09-252-991A-31777
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                                   GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING '
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR PILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: MATC J. Rubenfield et al.
APPLICANT: MATC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERBNCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,190
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR TILING DATE: 1998-07-27
NUMBER OF SEQ ID NO 18605
SEQ ID NO 18605
LENGTH: 778
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SEQ ID NO 31777
LENGTH: 67
                                                                                                                                                                                                                                                                                                            Sequence 31777, Application US/09252991A Patent No. 6551795
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Best Local (
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Best Local
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Local Similarity 100.0%; Pred. No. 25
1es 8; Conservative 0; Mismatches
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8, Conserve
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TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-5099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Pseudomonas aeruginosa US-09-252-991A-31777
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                                                                                                                                                                 NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 20965
LENGTH: 90
TYPE: PRT
ORGANISM: Pseudomonas seruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: GARY L. BETCON et al.
APPLICANT: GARY L. BETCON et al.
TITLE OF INVENTION: NUCLEIC ACID AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 2.0%; Score 7; DB 4; Best Local Similarity 100.0%; Pred. No. 28; Matches 7; Conservative 0; Mismatches
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Patent No. 6562958
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TITLE OF INVENTION: NUCLEIC ACID AND ANINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

PILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-02-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Patent No.
                                                                                                                                                                                                                                                                 PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
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5. 6551795
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                                     9 PAGSLSR 15
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                                                                         Similarity 7; Conserv
 PAGSLSR
                                                                           Conservative
                                                                         2.0%; Score 7; DB 100.0%; Pred. No. 34
                                                                                           DB 4;
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US-09-384-162-16; Sequence 16; Ap

Application US/09384162

RESULT 7

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US-09-252-991A-17117
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Sequence 17117, Application US/09252991A

Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
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APPLICANT: Malik, Kamal
APPLICANT: Malik, Kamal
APPLICANT: Malik, Kamal
APPLICANT: Malik, L., Brian
TITLE OF INVENTION: No. 6376747el Plant-Derived Map Kinase Kinase
FILE REFERENCE: 08-84280US
CURRENT APPLICATION NUMBER: US/09/384,162
CURRENT APPLICATION NUMBER: US/09/384,162
CURRENT PILING DATE: 1999-08-27
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS:
SEQ ID NO 24993
LENGTH: 146
TYPE: PRT
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Best Local Similarity 100
Matches 7; Conservative
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
PRIOR FILING DATE: 1998-07-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 133
TYPE: PRT
ORGANISM: Arabidopsis thallana
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nes 7; Conservative (
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100.0%; Pred. No. 48;
tive 0; Mismatches
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; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-17117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Homo sapiens
US-09-482-273-211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/482,273
CURRENT FILING DATE: 2000-01-13
EARLIER APPLICATION NUMBER: PCT/US99/15849
EARLIER FILING DATE: 1999-07-14
EARLIER FILING DATE: 1999-07-15
EARLIER FILING DATE: 1999-07-15
EARLIER APPLICATION NUMBER: 60/092,921
EARLIER APPLICATION NUMBER: 60/092,922
EARLIER APPLICATION NUMBER: 60/092,925
EARLIER APPLICATION NUMBER: 60/092,926
EARLIER APPLICATION NUMBER: 60/092,956
EARLIER FILING DATE: 1998-07-15
EARLIER FILING DATE: 1998-07-15
EARLIER FILING DATE: 1998-07-15
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                                                                                                                                                                                                                                                                                             Patent No. 5843749
GENERAL INFORMATION:
APPLICANT: Maisonni
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SEQ ID NO 17117
LENGTH: 153
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SEQ ID NO 211
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Patent No. 653463
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Rosen et al.
TITLE OF INVENTION: 71 Human Secreted Proteins
FILE REFERENCE: PZ030P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 160
TYPE: PRT
                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                       APPLICANT: Maisonpierre, et al.
TITLE OF INVENTION: EHK AND ROR TYROSINE
TITLE OF INVENTION: KINASES
                                                                                                                                                        STREET: 777 Old CITY: Tarrytown STATE: NY
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
JRRENT APPLICATION DATA:
                                                        COMPUTER:
                                                                                                                      ZIP:
                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                 ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         109 PLAAPAG 115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 PPCLLPL 9
                                                                                                                      10591
                                                                                                                                                                                             B: Regeneron Pharmaceuticals, Inc.
777 Old Saw Mill River Road
                                                                                                                                    U.S.A.
                                                    IBM Compatible
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: 107
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US/08/469,537A

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Sequence 23665, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:
APPLICANT: Maxc J. Rubenfield et al.
TITLE OP INVENTION: NUCLEIC ACID AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OP INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.136

CURRENT FILING DATE: 1999-02-18

CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR PILING DATE: 1998-07-27

NUMBER OF SEQ ID NO.33665

LENGTH: 167

TYPE: PRT
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                                                                         RESULT 13
US-08-469-537A-35
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US-09-252-991A-23665
               Sequence 35, Application US/08469537A Patent No. 5843749
GENERAL INFORMATION:
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Best Local Similarity 100.0%; Pred. No. 58
Matches 7; Conservative 0; Mismatches
                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIPICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/406,247
PILING DATE: 17-MAR-1995
APPLICATION NUMBER: USSN 08/144,992
PILING DATE: 28-OCT-1993
APPLICATION NUMBER: USSN 07/736,559
PILING DATE: 26-JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: KEMPILY DATE GAIL M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEX:
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
SEQUENCE 163 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS: single TOPOLOGY: unknown MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Kempler Ph.D., Gail M
REGISTRATION NUMBER: 32,43
REFERENCE/DOCKET NUMBER: REG 070C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 914-345-7400
 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: PILING DATE: 06-JUN
                                                                                                                                                                                                                                              Local
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                                                                                                                                                     112 POPRLPP 118
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                                                                                                                                                                                    39 POPRLPP 45
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Maisonpierre,
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FastSEQ Version 2.0

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RESULT 14
US-08-469-537A-36
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PILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/406,247
PILING DATE: 17-MAR-1995
APPLICATION NUMBER: USSN 08/144,992
PILING DATE: 28-JUL-1993
APPLICATION NUMBER: USSN 07/736,559
PILING DATE: 26-JUL-1991
ATTONNEY/AGENT INFORMATION:
NAME: Kempler, Ph.D., Gail M
REGISTRATION NUMBER: 32,143
REFERENCES/DOCKET NUMBER: REG 070C
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1943-945-7721
                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Maison
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COMPUTER: IBM Compatible ODERATING SYSTEM: DOS SOFTWARE: PABLISM V
                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: EH
TITLE OF INVENTION: KI
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Regeneron Pharmaceuticals, Inc
STREET: 777 Old Saw Mill River Road
                                                                                                                                                                                                                                                  TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: unknown MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: FASTSEQ Version 2.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 100.0%; Score 7; DB 2; local Similarity 100.0%; Pred. No. 67; les 7; Conservative 0. wires
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 190 amino acids
TYPE: amino acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 777 Old CITY: Tarrytown
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                                                                                                            ZIP: 10591
                                                                                                                                                                CITY: Tarrytown
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777 Old Saw Mill River Road
                                                                                                                                                                                                                                                                                          Maisonpierre, et
NVENTION: EHK AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       U.S.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EHK AND ROR TYROSINE KINASES
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ROR TYROSINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 190,
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US-08-444-083-8
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TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-469-537A-36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 8, Application US/08444083
Patent No. 5571675
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                        COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb flops
MEDIUM TYPE: 5.25 inch, 360 Kb flops
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: patin (Genentech)
CURREY APPLICATION DATA:
APPLICATION UMMBER: US/08/444,083
FILING DATE: 17-MAY-1995
CLASSIFICATION 1435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/233609
FILING DATE: 25-APR-1994
PRIOR APPLICATION UMBER: 08/286304
PRILING DATE: 05-AUG-1994
PRIOR APPLICATION UMBER: 08/286304
PRILING DATE: 05-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: TOSCH'S TEACHERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,537A
PILING DATE: 06-JUN-1995
CLASSIFICATION: 435
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/406,247
PILING DATE: 17-MAR-1995
PILING DATE: 17-MAR-1995
PILING DATE: 26-CT-193
APPLICATION NUMBER: USSN 07/736,559
PILING DATE: 26-JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: Kempler: Ph.D., Gail M
REGISTRATION NUMBER: 32,143
REFERENCE/DOCKET NUMBER: REG 070C
TELECOMOUNICATION INFORMATION:
TELEPHONE: 914-345-7400
TELEPAX: 914-345-7721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
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SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Baker, Joffre APPLICANT: Chien, Kenneth APPLICANT: King, Kathleen APPLICANT: Pennica, Diane APPLICANT: Wood, William APPLICANT: Wood, W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                103 DVWSLGV 109
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Torchia, Timothy B.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        360 Kb floppy disk
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REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: 894PID5
TELECOMMUNICATION INFORMATION:
TELESPAND: 415/25-8674
TELESPAN: 415/952-9881
TELESX: 910/371-7168
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 201 amino acids
TYPE: amino acids
US-08-444-083-8

Query Match
Best Local Similarity 100.0%; Score 7; DB 1; Length 201;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 7; Conservative 0; Mismatches 0; Gaps
Qy 282 AGLSAPA 288
US-08-494-083-8

Qy 282 AGLSAPA 75

Search completed: January 15, 2004, 15:07:22
Job time: 22 secs
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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Scoring table:
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                222222211111110
22222221111111111
225422109
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             200 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 500 - 
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seq length: 2000000000
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Match
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1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*

2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*

3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*

4: /cgn2_6/ptodata/1/iaa/FCTUS_COMB.pep:*

5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

6: /cgn2_6/ptodata/1/iaa/backfIles1.pep:*
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          GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd
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          B
     US-09-509-902A-9
US-09-878-989-15
US-08-878-989-15
US-08-557-006C-43
US-09-930-181-2
US-09-930-181-2
US-09-857-224B-19
US-08-688-988-29
US-08-688-988-29
US-08-688-988-29
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US-08-749-902-5
US-08-749-902-5
US-08-749-902-5
US-08-749-902-5
US-08-838-29-1
US-09-505-744-2
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(without alignments)
721.299 Million cell updates/sec
Sequence 9, Appli
Sequence 15, Appl
Sequence 24, Appli
Sequence 26, Appli
Sequence 26, Appli
Sequence 27, Appli
Sequence 29, Appli
Sequence 29, Appli
Sequence 19, Appli
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Sequence 1, Appli
Sequence 2, Appli
Sequence 3, Appli
Sequence 4, Appli
Sequence 4, Appli
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Sequence 17, Appli
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B 8	D	B 8	p Q	D Q	D Q	Query Best Matcl	RESULT US-09-09-09-09-09-09-09-09-09-09-09-09-09-		444400007600000000000000000000000000000
301 AERLTATGILLHPWLRQD 318 	241 AADVWSLGVALFTMLAGHYPFQDSEPVLLFGKIRRGAYALPAGLSAPARCLVRCLLRRE 283 AADVWSLGVALFTMLAGHYPFQDSEPVLLFGKIRRGAYALPAGLSAPARCLVRCLLRRE	181 RDLKLCRFVFADRERKKLVLENLEDSCVLTGPDDSLWDKHACPAYVGP)	121 ARPTEVLAGTOLLYAFFTRTHGDMHSLVRSRHRIPEBEAAVLFRQMATALAHCHQHGLVL 	61 AVATASRLGPYVLLEPEEGGRAYRALHCPTGTEYTCKVYPVQEALAVLEPYARLPPHKHV 	1 MRATPLAAPAGSLSRKKRLELDDNLDTERPVQKRARSGPQPRLPPCLLPLSPPTAPDRAT	ry Match 88.6%; Score 1675; DB 4; Length t Local Similarity 99.7%; Pred. No. 9.9e-164; ches 317; Conservative 1; Mismatches 0; Indels	RESULT 1 US-09-509-902A-9 ; Sequence 9, Application US/09509902A Patent No. 6387676 ; Patent No. 6387676 ; GENERAL INFORMATION: ; APPLICANT: Virca, Duke ; APPLICANT: Bird, Timothy A. ; APPLICANT: Handerson, Dirk M. ; APPLICANT: Anderson, Dirk M. ; APPLICANT: Human cDNAs Encoding Polypeptides Having FILE OF INVENTION: Human cDNAs Encoding Polypeptides Having FILE REFERENCE: 2877-US ; CURRENT APPLICATION UNMBER: US/09/509,902A ; CURRENT PILING DATB: 1999-08-03 ; NUMBER OF SEQ ID NOS: 16 ; SOFTWARE: PatentIN Ver. 2.0 ; SEQ ID NO 9 ; LENGTH: 360 TYPE: PRT ; ORGANISM: Homo sapiens US-09-509-902A-9	ALIGNMENTS	8 243 12.9 416 2 US-08-034-108-2 9 243 12.9 464 1 US-08-252-995D-6 1 243 12.9 464 2 US-08-834-108-6 1 243 12.9 925 1 US-08-834-108-4 2 243 12.9 925 2 US-08-834-108-4 2 442.5 12.8 351 3 US-08-688-988-28 241 12.7 295 3 US-08-689-988-23 1 12.7 295 2 US-08-499-448A-23 241 12.7 295 3 US-08-499-448A-23 1 12.7 295 3 US-08-499-4448-23 1 12.7 295 3 US-08-499-444-23 1 12.7 295 3 US-08-499-444-23 1 12.7 295 3 US-08-499-444-23 1 12.7 295 3 US-08-499-101-146-1 240 12.7 776 4 US-09-523-899-3 241 12.7 395 3 US-08-499-34 241 12.7 395 3 US-08-499-344-23 1 240 12.7 776 4 US-09-523-899-3 2 239 12.6 345 3 US-09-101-146-1 2 235.5 12.5 463 2 US-08-459-448A-25
	ARCLVRCLLRREP ARCLVRCLLRREP	PBILSSRASYSGK PBILSSRASYSGK	TALAHCHOHGLVL TALAHCHOHGLVL	LEPYARLPPHKHV EPYARLPPHKHV	LPLSPPTAPDRAT PLSPPTAPDRAT	360; 0; Gaps	Kinase		Sequence 2, Appl. Sequence 6, Appl. Sequence 4, Appl. Sequence 24, Appl. Sequence 28, App. Sequence 31, App. Sequence 23, App. Sequence 24, Appl. Sequence 25, App. Sequence 25, App. Sequence 26, App. Sequence 27, App. Sequence 27, App. Sequence 28, App. Sequence 29, App. Sequence 29, App. Sequence 20, App. Sequence 25, App. Sequence 25, App.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Guegler, Karl G.
APPLICANT: Lal, Preeti
APPLICANT: Goli, Surya K.
APPLICANT: Shah, Purvi
APPLICANT: Shah, Purvi
TITLB OP INVENTION: DISEASE A
TITLE OP INVENTION: KINASES
NUMBER OF SEQUENCES: 21
                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDENNESS: sing
STRANDENNESS: sing
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 1827450
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASESEQ for Windows Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/878,989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
ATTORNBY/AGENT INFORMATION:
NAME: Billings, Lucy J J
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0321 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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STATE: CA
COUNTRY: USA
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172 EPPEQR -- KKTICGTPNYVAPEVILRQG -- HGPEADVWSLGCVMYTLLCGSPPFETADLK 227
                                    210
                                                                           114
                                                                                                 150 SRHRIPEPEAAVLFROMATALAHCHOHGLVLRDLKLCRFVFADRERKKLVLENLEDSCVL
                                                                                                                                                                                        102 QEALAVLEPYARLP------PHKHVARPTEVLAGTQLLYAFFTR-THGDMHSLVR 149
                                                                                                                                                  57 SR---VAKPHOREKILNEIELHRDLOHRHIVRFSHHFEDADNIYIFLELCSRKSLAHIWK 113
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5885803
                                    TGPDDSLWDKHAC--PAYVGPEILSSRASYSGKAADVWSLGVALFTMLAGHYPFQDSEPV 267
                                                                           ARHTLLEPEVRYYLROILSGLKYLHORGILHRDLKLGNFFIT--ENMELKVGDFGLAARL
                                                                                                                                                                                                                                 LPTSDPGRLITDPRSGRTYLKGRLLG------KGGFARCYEATDTETGSAYAVKVIPQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3B: Incyte Pharmaceuticals, Inc
3174 Porter Drive
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Guegler, Karl G.
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Hillman, Jennifer L.
Corley, Neil C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15:
                                                                                                                                                                                                                                                                                                            45; Mismatches 129;
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US-09-272-796-15
Sequence 15, Application US/09272796
Patent No. 6207148
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; CLONB: 1827450
US-09-272-796-15
                                                                                                                                           Matches
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                      TELEX:
INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION NUMBER: 08
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J J
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PP-0321
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                TOPOLOGY: line
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                     LENGTH: 607 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatik
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: DOS
SOFTWARE: PASESEQ for Windows Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/272,796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Bandman, Olga
APPLICANT: Hilman, Jennifer L.
APPLICANT: Corley, Neil C.
APPLICANT: Guegler, Karl G.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
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CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                             TELEPAX: 415-845-4166
                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
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                                 102 QEALAVLEPYARLP------PHKHVARPTEVLAGTQLLYAFFTR-THGDMHSLVR 149
                                                                                                                                         92;
                                                                                                    48 LPLSPP----TAPDRATAVATASRLGPYVLLEPEEGG--RAYRALHCPTGTEYTCKVYPV 101
SR---VAKPHQREKILNEIELHRDLQHRHIVRFSHHFEDADNIYIFLELCSRKSLAHIWK 113
                                                                    LPTSDPGRLITDPRSGRTYLKGRLLG------KGGFARCYBATDTBTGSAYAVKVIPQ 56
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Shah, Purvi
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                                                                                                                                     15.4%; Score 290.5; DB 3; 29.2%; Pred. No. 3.4e-21; tive 45; Mismatches 129;
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                                                                                                                                         Indels 49;
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; LOCATION: (1)..(633)
; OTHER INFORMATION: Yeast SNF1 polypeptide
US-08-557-006C-43
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US-08-557-006C-43
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SOFTWARE: Patentin V.
SEQ ID NO 43
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PRIOR FILING DATE: 1994-05-20
PRIOR APPLICATION NUMBER: GB 9310489.1
PRIOR FILING DATE: 1993-05-21
PRIOR APPLICATION NUMBER: GB 9318010.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Beri, Rajindar K.
APPLICANT: Carling, David
APPLICANT: Forder, Robert A.
TITLE OF INVENTION: NUCLEIC ACID ENCODING AMP-ACTIVATED PROTEIN KINASE
FILE REFERENCE: NUGAP/PHM37588/UST
CURRENT APPLICATION NUMBER: US/08/557,006C
CURRENT APPLICATION NUMBER: US/08/557,006C
CURRENT FILING DATE: 1996-03-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Yeast
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ENGTH: 633
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                                  268
                                                                       277
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                                                                                                                                                                             154 ARREFQQIISAVEYCHRKIVHRDLKPENLLLDEHLNVKIADFGL--SNIMT---DGNFL
336 VPDGLGLDEAREEEGD 351
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                                  VYTLPKFLSPGAAGLIKRMLIVNPLNRISIHEIMQDDWFKVDLPEYLLP------
                                                                                                        KTSCGSPNYAAPEVISGKL-YAGPEVDVWSCGVILYVMLCRRLPPDDESIPVLPKNISNG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PatentIn Ver. 2.1
                                                                 AYALPAGLSAPARCLVRCLLRREPAERLTATGILLHPWLRQD-PMPLAPTRSHLWEAAQV
                                                                                                                                                                                                                                                       SDMQGRIEREISYLRLLRHPHIIKLYDVIKSKDBIIMVIBYAGNELFDYIVQRDKMSEQB
                                                                                                                                                                                                                                                                                                                              SNSTLNNPKSSLADGAHIGNYQIVKTLGEGSFGKVKLAYHTTTGQKVALKIIN-KKVLAK 93
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                                                                                                                                                                                                                                                                                                                                                                                                                       14.5%; Score 274.5; DB 3; 27.8%; Pred. No. 1.6e-19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 633;
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US-07-857-224B-26
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US-09-930-181-2
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LENGTH: 668
TYPE: PRT
                                                                                                                                                                                                                                                                             Sequence 26, Application US/07857224B Patent No. 5958784
GENERAL INFORMATION:
APPLICANT: Benner, Steven A.
TITLE OF INVENTION: Predicting Fo
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APPLICANT: OriGene Technologies
TITLE OF INVENTION: Full-Length Serine Protein Kinase in Brain and Pancreas
FILE REFERENCE: 16U 101 V1
CURRENT APPLICATION NUMBER: US/09/930,181
CURRENT FILING DATE: 2001-08-16
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Homo sapiens
                                                                                ZIP: (note: this is an international post code)
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette, 1.4 Mb storage
                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Steven A. Benner
STREET: Hadlaubstrasse 151
                 SOPTWARE: Microsoft Word CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                   COMPUTER: Apple MacIntosh OPERATING SYSTEM: MacIntosh 7.0
APPLICATION NUMBER:
                                                                                                                                               STATE: none
COUNTRY: Switzerland
                                                                                                                                                                                       CITY: Zurich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    243
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 US/07/857,224B
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Pred. No. 2.2
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GENERAL INFORMATION:
APPLICANT: Lefebvre, Daniel D.
APPLICANT: Malboobi, Mohammad A.
APPLICANT: Malboobi, Mohammad A.
TITLE OF INVENTION: PHOSPHATE STARVATION-INDUCIBLE PROTEINS
PILE REFERENCE: PPL96-03
CURRENT APPLICATION NUMBER: US/08/688,988B
CURRENT FILING DATE: 1996-07-31
NUMBER OF SEQ ID NOS: 48
SOFTMARE: FASESEQ for Windows Version 3.0
SEQ ID NO 33
LENGTH: 339
TYPE: PRT
ORGANISM: Glycine max
US-08-688-988-33
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; VOLUME: 241
; PAGES: 42-52
; DATE: 1988
US-07-857-2248-26
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US-08-688-988-33
/ Sequence 33, Application US/086889888
/ Patent No. 6096545
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INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 252
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE:
DESCRIPTION: protein
ORIGINAL SOURCE:
ORGANISM: Schizosaccharomyces pombe
FEATURE: Protein kinase; Table 8 Column 29
Query Match 14.0%; Score 265.5; DB 3; Best Local Similarity 28.7%; Pred. No. 5.5e-19; Matches 86; Conservative 35; Mismatches 86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 14.2%; Score 268.5; DB 2; Best Local Similarity 31.5%; Pred. No. 1.8e-19; Matches 74; Conservative 44; Mismatches 108;
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CLASSIFICATION: 436
PRIOR APPLICATION DATA: none
TELECOMMUNICATION INFORMATION:
TELEPHONE: (International) 41 1
TELEPAX: (International) 41 1
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AUTHORS: Hanks, S. K.
AUTHORS: Quinn, A. M.
AUTHORS: Hunter, T.
AUTHORS: Hunter, T.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AKHAKTGDLAAIKIIPIRYASIGMEILMMRLLRHPNILRLYDVWTDHQHMYLALEYVPDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FGGQNTDVIYNKIRHGAYDLPSSISSAAQDLLHRMLDVNPSTRITIPEFFSHPFL 249
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262 2437
  Indels 93;
                                      Length 339;
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Gapa
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07-857-224B-19	US-C
DAT	
241	
TITLE: The protein kinase family JOURNAL: Science	٠. ٠.
S: Hunter, T.	٠. ٠
AUTHORS: Hanke, S. K. AUTHORS: Ouinn, A. M.	 -
FRATURE: Protein kinase; Table 8 Column 21	
SM: rat	٠. ٠
ORIGINAL SOURCE:	
	.
TOPOLOGY: linear	
H: 264	
CHARACTERISTICS:	
INFORMATION FOR SEC ID NO: 19:	. .
X: (International) 41 1 262 24	
3	
CLASSIFICATION: 436	
TION NU	. . .
Ä	
SOFTWARE: Microsoft Word	·. •.
Apple MacIntosh	٠.
TYPE: 3.5	٠. ٠
ZIP: (note: this is an international post code) CH-8092	
Y: Switzerland	٠.
STATE: none	•• ••
TREET:	
ADDRESSEE: Steven A. Benner	٠. ٠
NUMBER OF SEQUENCES: 114	·· ··
OF INVENTION: P	٠.
CANT: Benner, Steven A.	٠
ყ:	
8 8 6	RESULT US-07-
272 AERRGYEETQKDQPSQSVEEIMQIIQEARTKIHTGEQAGTGTSDVVRGDEANEEV 326	8
323APTRSHLWEAAQVVPDGLGL-DEARBEEGDREV 354	S
212 KSIGKIMSVQTAIFUTVKVSKECKHLISKIFVANFAKKINISBIRQHLWFKKNLFKBIIB 2/I	מ
	2
271GKIRRGAYALPAGLSAPARCLVRCLLRREPAERLTATGILLHPWLRQD-PMPL 322	S
164PAYIAPEVL-SRKBYDGKVADVMSCGVTLYVMLVGAYPFBDPEDPKNPR 211	문
GPEILSSRASYSGKAADVWSLGVALFTMLAGHYPF	Ş
109 ISGVSYCHSMQICHRDLKLENTLLDGNPAPRLKICDFGFSKSALLHSQPKSTVGT- 163	문
167 ATALAHCHQHGLVLRDLKLCRFVFADRERKKLVLENLEDSCVLTG 211	ঠ
IIRFKEVFLTPTHLAIVLEYAAGGELFERICNAGRLSEDEARFFF	문
11) HKHVAKPIBVLAGTQLLYAFFIRTHGUMHSUVXSKHKIFBFBAAVLFRQM 100	Ş

Query Match

13.9%;

Score 263.5;

DB 2;

Length 264;

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RESULT 9
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                                                                                                                                                                                                                                                                            INFORMATION POR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 257
TYPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 25, Application US/07857224B
Patent No. 5958784
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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                                                                                                                                     DESCRIPTION: protein
ORIGINAL SOURCE:
ORGANISM: Saccharomyces cerevisiae
FEATURE: protein kinase; Table 8 Column 28
PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA: none TELECOMMUNICATION INFORMATION: TELEPHONE: (International) 41 1 632 2830 TELEPAX: (International) 41 1 262 2437
                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOPTWARE: Microsoft Word
CURRENT APPLICATION DATA:
APPLICATION US/07/857,224B
APPLICATION UMBER: US/07/857,224B
PILING DATE: 03/25/92
CLASSIPICATION: 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: (note: this is an international post code) CH-8092
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette, 1.4 Mb storage
COMPUTER: Apple MacIntosh
OPERATING SYSTEM: MacIntosh 7.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Benner, Steven A. TITLE OF INVENTION: Predicti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 1: CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                         MOLECULE TYPE:
                  AUTHORS: Hanks, S. K.
AUTHORS: Quinn, A. M.
AUTHORS: Hunter, T.
TITLB: The protein kinase
JOURNAL: Science
JOURNAL: SC
VOLUME: 241
                                                                                                                                                                                                                                                                        TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                          TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Zurich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Steven A. Benner
STREET: Hadlaubstrasse 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               311
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         196 KKLV-LENLEDSCVLTGPDDSLWDKHACPAYVGPEILSSRASYSGKAADVWSLGVALFTM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 84 RALHCPTGTEYTCKVYPVQEALA----VLEPYA----RLPPHKHVARPTEVLAGTQLLYAF 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        74; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LVGYPPFWDEDQHKLYQQIKAGAYDFPSPEWDTVTPEAKNLINQMLTINPAKRITAHEAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KHPWVCQ 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LHPWLRQ 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LAGHYPFQDSEPVLLFGKIRRGAYALPA----GLSAPARCLVRCLLRREPAERLTATGIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FTR-THGDMHSLVRSRHRIPEPEAAVLFRQMATALAHCHQHGLVLRDLKLCRFVFADRER 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FDLVTGGELFEDIVAREYYSEADASHCIQQILEAVLHCHQMGVVHRDLKPENLLLASKLK 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           none
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Switzerland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Predicting
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                                                                                                                                                                                                                                                                                                                                       25:
                                           family
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15; Gaps
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APPLICANT: Carling, David

APPLICANT: Forder, Robert A.

APPLICANT: Forder, Robert A.

ITITLE OF INVENTION: NUCLEIC ACID ENCODING AMP-ACTIVATED PROTEIN KINJ

FILE REFERENCE: NGAP/PHM37588/UST

CURRENT APPLICATION NUMBER: US/08/557,006C

CURRENT FILING DATE: 1996-03-06

PRIOR APPLICATION NUMBER: CT/GB94/01093

PRIOR APPLICATION NUMBER: GB 9310489.1

PRIOR APPLICATION NUMBER: GB 9310489.1

PRIOR APPLICATION NUMBER: GB 931010.7

PRIOR APPLICATION NUMBER: GB 931010.7

PRIOR APPLICATION NUMBER: GB 9310010.7

PRIOR PILING DATE: 1993-08-31

NUMBER OF SEQ ID NOS: 44

NOMBER OF SEQ ID NOS: 44
                                                                                                                                                                                                                                                                                                                                                              TYPE: PRI
; TYPE: PRI
; ORGANISM: Rat
; PRATURE:
; NAME/KEY: gene
; LOCATION: (1)...(1747)
; OTHER INFORMATION: Full length cDNA sequence fragment of Human AMPK -
; OTHER INFORMATION: fragment begins at nucleotide 24 and ends with
; OTHER INFORMATION: nucleotide 1765
US-08-557-006C-40
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US-08-557-006C-40
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SEQ ID NO 40
LENGTH: 552
                                                                                                                                                                                                                                                                          Query Match 13.8
Best Local Similarity 29.2
Matches 82; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 40, App. Patent No. 62585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Beri, R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 13.9%; Score 263; DB 2; Length 25
Best Local Similarity 28.8%; Pred. No. 6.6e-19;
Matches 72; Conservative 43; Mismatches 117; Indels
175 QHGLVLRDLKLCRFVFADRERKKLV---LEN-----LEDSCVLTGPDDSLWDKHACPA 224
                                                                                                                         116 PHKHVARPTSVLA-GTQLLYAFFTRTHGDMHSLVRSRHRIPBPBAAVLFROMATALAHCH 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     188 VILYVMLCRRLPFDDESIPVLFKNÍSNGVÝTLPKFLSPGAAGLIKRMLIVNPLNRISIHE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    249 VALFTMLAGHYPFQDSEFVLLFGKIRRGAYALPAGLSAPARCLVRCLLRREPAERLTATG 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         134 DEHLNVKIADFGL--SNIMT---DGNFLKTSCGSPNYAAPEVISGKL-YAGPEVDVWSCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        191 ADRERKKLVLENLEDSCVLTGPDDSLWDKHAC--PAYVGPEILSSRASYSGKAADVWSLG 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       131 QLLYAFFTRTHGDMHSLVRSRHRIPEPBAAVLFRQMATALAHCHQHGLVLRDLKLCRFVF 190
                                                                                                                                                                                                                       67 RLGPYVL---LEPEEGGRAYRALHCFTGTEYTCKVYPVQE--ALAVLEPYAR-----LP
                                                                                                                                                                           12 KIGHYVLGDTLGVGTFGKVKIGEHQLTGHKVAVKILNRQKIRSLDVVGKIKREIQNLKLF 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15 GKVKLÁYHTTTGQKVALKIIN-KKVLÁKSDMQGRIERBISÝLŘÍLRHPHIIKLYDVIKSK 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           74 DEIIMVIEYAGNELFDYIVQRDKMSEQEARRFFQQIISAVEYCHRHKIVHRDLKPENLLL 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           80 GRAYRALHCPTGTEYTCKVYPVQEALAVLE------PYARLPPHKHVARPTEVLAGT 130
                                                                         RHPHIKLYQVISTPTDFFMVMEYVSGGELFDYICKHGRVEEVBARRLFQQILSAVDYCH 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PatentIn Ver.
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                                                                                                                                                                                                                                                                                                       13.8%;
                                                                                                                                                                                                                                                                               43;
                                                                                                                                                                                                                                                                            Score 260.5; DB 3;
Pred. No. 3.6e-18;
43; Mismatches 119;
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                                                                                                                                                                                                                                                                            Indels 37;
                                                                                                                                                                                                                                                                                                                              Length 552;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18;
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RESULT 12
US-07-857-2248-18
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US-08-688-988-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 48
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 29
LENGTH: 354
TYPE: PRT
ORGANISM: Brassica napus
US-08-688-988-29
                                                                                                                            Patent NO. 3777.

GENERAL INFORMATION:

APPLICANT: Benner, Steven A.

TITLE OF INVENTION: Predicting Folded Structures of Proteins
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:

ADDRESSE: Steven A. Benner

undlaubstrasse 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Lefebvre, Daniel D.
APPLICANT: Malboobi, Mohammad A.
APPLICANT: NUMBER OF INVENTION: PHOSPHATE STARVATION-INDUCIBLE PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 29, Appli
Patent No. 6096545
                                                                                                                                                                                                                                                                                                                          Sequence 18, Application US/07857224B Patent No. 5958784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 13.5%; Score 256; DB 3; Length 354; Best Local Similarity 29.5%; Pred. No. 5.5e-18; Matches 86; Conservative 32; Mismatches 104; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/08/688,988B CURRENT FILING DATE: 1996-07-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE: PPL96-03
COUNTRY: Switzerland
ZIP: (note: this is an international post code) CH-8092
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette, 1.4 Mb storage
COMPUTER: Apple MacIntosh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       220
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               176 HGLVLRDLKL-------CRFVFADRERKKLVLENLEDSCVLTGPDDSLWDKH 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      117 HKHVARPTE-VLAGTQLLYAFFTRTHGDMHSLVRSRHRIPEPEAAVLFRQMATALAHCHQ 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 238 NRSIATLLMHMLQVDPLKRATIKDIREHEWFKQDLPSYLPP 278
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                280 ENPTFSPQTAEEIMKIVDDAKTPPPVSRSIGGFGWGGKGDEEEEEVDBEEVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  277 AYALP--AGLSAPARCLVRCLLRREPAERLTATGILLHPW-LRQDPMPLAPTRSHLW---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         221 ACPAYVGPEILSSRASYSGKAADVWSLGVALFTMLAGHYPFQDSEPVLLF----GKIRRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            57 HPNIIRFKEVVLTPTHLAIAMEYAAGGELFERICSAGRESEDEARYFFQQLISGVSYCHA 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----EAAQVVPD---
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                                                                                                                       none
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Application US/08688988B
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US-08-913-050A-7
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Matches
                                                                                                                                                                                                                                                      Sequence 7, Application US/08913050A Patent No. 5827726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: NEZU, JU
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEX: none
INFORMATION FOR SEQ ID NO:
                                                                                                     NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NOTICE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/07/857,224B
PILING DATE: 03/25/92
CLASSIPICATION: 436
PRIOR APPLICATION DATA: none
TELECOMMUNICATION INFORMATION:
TELEPHONE: (International) 41 1 632 2830
TELEPHONE: (International) 41 1 262 2437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE: Protein kinase; Table 8 Column PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PAGES: 42-9
DATE: 1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AUTHORS: Hunter, T. TITLE: The protein kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: MacIntosh SOFTWARE: Microsoft Word
                                                   STATE:
                                                                    CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JOURNAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AUTHORS: Hanks, S. K. AUTHORS: Quinn, A. M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid TOPOLOGY: linear
                              COUNTRY:
                                                                                                STREET:
       ZIP: 20004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          122 VHRDLKPENLLLASKLKGAAVKLADFGLAIEVEGEQQAWFGFAGTFGYLSPEVL--RKDP 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    179 VLRDLKLCRFVFADRERKKLV-LENLEDSCVLTGPDDSLWDKHACPAYVGPEILSSRASY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              120 VARPTEVLAGTQLLYAFFTR-THGDMHSLVRSRHRIPBPBAAVLFRQMATALAHCHQHGL
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77; Conserv
                              f: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YGKPVDLWACGVILYILLVGYPPFWDEDQHRLYQQIKAGAYDFPSPEWDTVTPEAKDLIN 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YOLFE-BLGKGAPSVVRRCVKVLAGQEYAAKIINTKKLSARDHQKLBREARICRLLKHPN
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                                                                                           3B: BROWDY AND NEIMARK, P.L.L.C.
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                                                                                                                                                                                                                      Patent No. 5985635
GENERAL INFORMATION:
APPLICANT: Bandman
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REFERENCE/DOCKET NUMBER: NEZU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197
TELEPAX: (202) 737-5528
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                     Sequence 5,
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PILING DATE: 16-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP PCT/JP96/006
PILING DATE: 15-MAR-1996
ATTORNEY/ACENT INFORMATION:
NAME: YUN, Allen C.
                                                                                                                       APPLICANT: Bandman, Olga
APPLICANT: Goli, Surya K.
APPLICANT: Hillman, Jennifer L.
TITLE OF INVENTION: NOVEL HUMAN SERINE/THREONINE
TITLE OF INVENTION: PROTEIN KINASES
NUMBER OF SEQUENCES: 8
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STRANDEDNESS: single
TOPOLOGY: line
(OLECTION)
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MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEB: INCYTE PHARMACEUTICALS, INC
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: peptide
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                                CITY: Palo Alto
STATE: CA
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                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 287
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                                                                                                                                                                                                                                                                   , Application US/08749902 5985635
94304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HKHVARPTEVLAG--TOLLYAFFTRTHGDMHSLVRS--RHRIPEPEAAVLFROMATALAH 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                               KGMLEYEPAKRPSIRQIRQHSWPRKKHPPAEAPVPIPPSPDTKDRWRSMTVVPYLEDLHG 346
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Sequence 32, Application US/08688988B

Patent No. 6096545

GENERAL INFORMATION:
APPLICANT: Lefebvre, Daniel D.
APPLICANT: Malboobi, Mohammad A.
TITLE OF INVENTION: PHOSPHATE STARVATION-INDUCIBLE PROTEINS
FILE REFERENCE: PPL96-03
CURRENT APPLICATION NUMBER: US/08/688,988B
CURRENT FILING DATE: 1996-07-31
NUMBER OF SEQ ID NOS: 48
SOPTWARE: FRASESEQ for Windows Version 3.0
SEQ ID NO 32
LENGTH: 359
TYBE: PRT
ORGANISM: Brassica napus
US-08-688-988-32
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IMMEDIATE SOURCE:
LIBRARY: GenBar
CLONE: 1480861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: Filed Herewith PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOPTWARE: FASTSEQ Version 2.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett.
COMPUTER: IBM Compat:
OPERATING SYSTEM: DO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 433 amino TYPE: amino acid
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TOPOLOGY: lin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                             347
                                                                                                                                                                                                                                                                                                                                                                                                                                342 LDEAREBEGDREVVLY 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          293 RCLLRREPAERLTATGILLHPWLRQD-----PMPLAPTRSHLWEAAQVVP---DGLG 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   107 HKNVIQLVDVLYNBEKOKMYMVMEYCVCGMQEMLDSVPEKRPPVCQAHGYPCQLIDGLEY 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      233 SRASYSGKAADVWSLGVALFTMLAGHYPFQDSBPVLLFGKIRRGAYALPAGLSAPARCLV 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             167 LHSQGIVHKDIKPGNLLLTTGGTLKISDLGVAEALHPFAADDTCRTSQGSPAFQPPEIAN 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               173 CHQHGLVLRDLKLCRFVFADRERKKLVLENLEDSCVLTGPDDSLWDKHACPAYVGPEILS 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         117 HKHVARPTEVLAG--TQLLYAFFTRTHGDMHSLVRS--RHRIPEPEAAVLFRQMATALAH 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     70;
                                                                                                                                                                                                                                                                                                                                                                                             ADEDEDLFDIEDDIIY 362
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 252.5; DB 2;
Pred. No. 1.7e-17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PF-0150 US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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Query Match Best Local Matches 8	Query Match Best Local Similarity 28.6%; Pred. No. 3.7e-17; Matches 84; Conservative 33; Mismatches 105; Indels 72; Gaps 11;
ঽ	117 HKHVARPTE-VLAGTQLLYAPPTRTHGDMHSLVRSRHRIPEPEAAVLPRQMATALAHCHQ 175
90	57 HPNIIRFKEVVLTPTHLAIAMEYAAGGELFERICGAGRFSEDEARYFFQQLISGVSYCHA 116
Ś	176 HGLVLRDLKL
Db	117 MQICHRDLKLENTLLDGSPAPRLKICDFGYSKSSLLHSRPKSTVGT 162
ð	221 ACPAYVGPEILSSRASYSGKAADVWSLGVALFTMLAGHYPPQDSBPVLLFGKIRRG 276
gb dg	163 PAYIAPEVL-SRREYDGKWADVWSCGVTLYVMLVGAYPPEDQEDPKNPRKTIQKIMAV 219
ક	277 AYALPAGLSAPARCLVRCLLRREPAERLTATGILLHPWLRQD-PWPLAPTRSHLW 330
망	220 QYKIPDYVHISQDCKHLLSRIFVANSLKRITIAEIKKHPWFTKNLPRELTETAQAAYFKK 279
ð	331 ····EAAQVVPD·····GLG····-LDEAREEEGDREVV 355
DЬ	280 ENPTFSAQTAEEIMKIVDDAKTPPPVSRSIGGFGWGGEGDLEGKEEEEVDEEEV 333
Search completed: Job time : 22 secs	Search completed: January 15, 2004, 15:02:26 Job time : 22 mece

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Title:
Perfect score:
Sequence:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Searched:
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10916.435 Million cell updates/sec
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gb ba: *
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gb in: *
gb pat: *

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Pred. No. is the number of results predicted by chance to have a

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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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10016	0000114000	# I N N N W N W N W W W W W W W W W W W W	- BB
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ALIGNMENTS

AUTHORS	REFERENCE	OKGOUNTON		KEYWORDS	VERSION	ACCESSION		DEFINITION	Locus	BC019363	RESULT 1
Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,	Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 2121)	Rukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;	Homo sapiens (human)	MGC.	BC019363.1 GI:17939414	BC019363	MGC:854 IMAGE:3528490), complete cds.	eading frame 97, r	BC019363 2121 bp mRNA linear PRI 06-JUN-2003		

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REMARK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE
                                                                                                                                                                                                                                           gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                       source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Helsch, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., WcZwan, P.J., Malek, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villaion, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Villaion, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A. Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue procurement: ATCC
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consor
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
info@bcgsc.bc.ca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAL Plate: 8 Row: g Column: 5
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 11056039.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield, Susanna Chan, Readman Chiu, Chris Pjell, Erin Garland, Ran Guin, Letticia Haiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott, Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (13-DEC-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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Direct Submission
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/tlssue type="Muscle, rhabdomyosarcoma"
/clone Ibs="NHH MGC(17"
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                                                                                                                                 /codon
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VLFRQMATALAHCHQHKLVLRDLKLCRFVFADRERKKLVLENLEDSCYLTGPDDSLMD
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AYALPAGLSAPARCLYRCLLRREPAERLTATGILLHFMLRQDPMPLAFTRSHLMEAAQ
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a 645 c 584 g 433 t

Similarity GAGCCTGTCCTGCTCTTCGGCAAGATCCGCCGCGGGGCCTACGCCTTGCCTGCAGGCCTC GACTCCTGCGTGCTGACTGGGCCAGATGATTCCCTGTGGGACAAGCACGCGTGCCCAGCC CACAGCCTGGTGCGAAGCCGCCACCGTATCCCTGAGCCTGAGGCTGCCGTGCTCTTCCGC TTAGATACCGAGCGTCCCGTCCAGAAACGAGCTCGAAGTGGGCCCCAGACCGCCCAGACTGCCC TACGTGGGACCTGAGATACTCAGCTCACGGGCCTCATACTCGGGCAAGGCAGCCGATGTC TACGTGGGACCTGAGATACTCAGCTCACGGGCCTCATACTCCGGGCAAGGCAGCCGATGTC GACTCCTGCGTGCTGACTGGGCCAGATGATTCCCCTGTGGGACAAGCACGCGTGCCCAGCC GAGGTCCTGGCTGGTACCCAGCTCCTACGCCTTTTTCACTCGGACCCATGGGGACATG CTGGCCGTGCTGGAGCCCTACGCGCGCGCTGCCCCCGCACAAGCATGTGGCTCGGCCCACT GCCCTGCACTGCCCTACAGGCACTGAGTATACCTGCAAGGTGTACCCCCGTCCAGGAAGCC TGGAGCCTGGGCGCTCTTCACCATGCTGGCCGGCCACTACCCCTTCCAGGACTCG CTGTGTCGCTTTGTCTTCGCTGACCGTGAGAGGAAGAAGCTGGTGCTGGAGAACCTGGAG CAGATGGCCACCGCCCTGGCGCACTGTCACCAGCACGGTCTGGTCCTGGTGATCTCAAG CAGATGGCCACCGCCCTGGCGCACTGTCACCAGCACGGTCTGGTCCTGCGTGATCTCAAG CACAGCCTGGTGCGAAGCCGCCACCGTATCCCTGAGCCTGAGGCTGCCGTGCTCTTCCGC GAGGTCCTGGCTGGTACCCAGCTCCTCTACGCCTTTTTCACTCGGACCCATGGGGACATG CTGGCCGTGCTGGAGCCCTATGCGCGGCTGCCCCCGCACAAGCATGTGGCCTCGGCCCACT GCCCTGCACTGCCCTACAGGCACTGAGTATACCTGCAAGGTGTACCCCGTCCAGGAAGCC cccrecci CCCTGCCTGTTGCCCCTGAGCCCACCTACTGCTCCAGATCGTGCAACTGCTGTGGCCACT TTAGATACCGAGCGTCCCGTCCAGAAACGAGCTCGAAGTGGGCCCCAGCCCAGACTGCCC CCTCTGGCTGCTGCGGGTTCCCTGTCCAGGAAGAAGCGGTTGGAGTTGGATGACAAC CCTCTGGCTGCTGCGGGTTCCCTGTCCAGGAAGAAGCGGTTGGAGTTGGATGACAAC 459 Conservative 99.8**%**; <u>,</u> Score Pred. Mismatches ŏ. 2055.8; 0 뮵 ν γ. 9. Indels Length 0 Gape 899 959 900 840 839 660 600 60 780 779 720 659 599 540 539 480 479 420 419 360 359 300 299 240 239 180 120 119 179 0

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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyl
Yoon, V.S., Kowis, C.R., Lawrence, S., Mart:
Richards, S., Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
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Submitted (04-APR-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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Homo sapiens, chromosome 20 open reading
IMAGE:5104452, mRNA, complete cda
BC027484
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NIH-MGC Project URL: http://mgc.nci.nih.gov
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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KYALPAGLSAFARCLVRCLLRREPAERLTATGILLHFWLRQDPMPLAPTRSHLWEAAQ
                   VVPDGLGLDEARBEEGDREVVLYG"
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AK026945 AK026945 N Homo sapiens cDNA: FLJ23292 fis, clone HEP10334. AK026945 AK026945 AK026945.1 GI:10439923 oligo capping; fis (full insert sequence).	1991 GAATTATGAAATAAAAAAAAAAAAAAAAAAAAAAAAAA	67	07	01 ATGGGCTTCTGACCTGAGCACCAAGGTTGAGGGACAGGATTAGGCAGGGTCTGTCCTGT 	41 TGAGGCTAGTTCTTGTCTAACTCAAGACTGTTCTGGAATGAGGGTCCAGGCCTGTCAACC 	ANGAGATICTCCTTCCAGGCCTANGCCTGGGATTTGGGCCAGAGATAAGAATCCAAACTA AAAAAGATTCTCCTTCCAGGCCTAAGCCTGGGATTTGGGCCAGAGATAAGAATCCAAACTA	1 CAGGACCCAAGCCCAGCTCACTCTGGGAACTGTGTTCCCAGCATCTCTGTCCTCTTGATT 67 CAGGACCCAAGCCCAGCTCACTCTGGGAACTGTGTTCCCAGCATCTCTGTCCTCTTGATT 68 NAGACTTAGCTTGGGAACTGTGTTCCCAGCATCTCTGTCCTCTTGATT	61 CCTTTTCAGAGAAAGGAAGTTTCCCTGTGCCAAAGGCTCCAGGCCTCTCCCCTGCAACT	01 GGCACCTCTGTCCAAGGACAATCCCCTTTCACAAACAAAC	41 TCACTGTCTACACTGGGTACACTTTGTACCAGTGTTCGGCTCCACTGATGCTGGTGCTCA 87 TCACTGTCTACACTGGGTACACTTTGTACCAGTGTCGGCCTCCACTGATGCTGGTGCTCCACTGATGCTGATGCTGGTGCTCCACTGATGCTGGTGCTCCACTGATGCTGGTGCTCCACTGATGCTGGTGCTCCACTGATGCTGGTGCTCCACTGATGCTGGTGCTCCACTGATGCTGGTGCTCCACTGATGCTGGTGCTCCACTGATGCTGGTGCTCCACTGATGCTGGTGCTCCACTGATGCTGGTGCTCCACTGATGCTGGTGCTCCACTGATGCTGGTGCTCCACTGATGCTGGTGCTCCACTGATGCTGGTGCTCCACTGATGCTGGTGCTCCACTGATGCTGGTGCTCCACTGATGCTGGTGCTCCACTGATGCTGGTGCTCACTGATGCTGGTGCTCCACTGATGCTGGTGCTCACTGATGCTGGTGCTCCACTGATGCTGGTGCTCCACTGATGCTGGTGCTCACTGATGCTGGTGCTCACTGATGCTGGTGCTCACTGATGCTGGTGCTCACTGATGCTGGTGCTCACTGATGCTGGTGCTCACTGATGCTGGTGCTCACTGATGCTGGTGCTCACTGATGCTGGTGCTCACTGATGCTGGTGCTCACTGATGCTGGTGCTCACTGATGCTGGTGCTCACTGATGCTGGTGCTCACTGATGCTGGTGTGATGATGATGATGATGATGATGATGATGATGATG	TGCTCACAGAGATGACAAACTGGCATCCTTGAGCTGACAACACTTTTCCATGACCATAGG	21 GTGCCAAGCCCTGTTCTGGGTGCTGGGAGTACAGCAGTGAGCAAAGGAGACAATATTCCC 67 GTGCCAAGCCCTGTTCTAGGTGCTGGGAGTACAGCAGTGAGCAAAGGAGACAATATTCCC	TIGGTSTREACATCTGCTTTGTTCCACACACATGCAGTTCCTGCTTGGGTGCTTATCAG	THE TABLE TO THE T	THE CONTROL OF THE PROPERTY OF	1081 GCCAGGGAAGAGGAGGAGACAGAGAAGTGGTTCTGTATGGCTAGGACCACCCTACTACA 1140

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41 87	181 CCCTGCCTGTTGCCCCTGAGCCCACCTACTGCTCCAGATCGTGCAACTGCTGTGGCCACT 240	121 TTAGATACCGAGCGTCCCGTCCAGAAACGAGCTCGAAGTGGGCCCCAGCCCAGACTGCCC 180	61 CTTCTGGCTGCTGCGGGTTCCCTGTCCAGGAAGAGCGGTTGGATGACAAC 120	1 GCTCTGAGCCCCGGCCCGGGCCCACGCGGAACGACGGGGCGAGATGCGAGCCACC 60	Query Match 97.3%; Score 2003; DB 9; Length 2257; Best Local Similarity 99.8%; Pred. No. 0; Matches 2006; Conservative 0; Mismatches 5; Indels 0; Gaps 0;	AYALPAGLSAPARCLVRGLLRREPABRLTATGILLHPWLRQDPMPLAPTRSHLWEAAQ VVPDGLGLDEAREEEGDREVVLYG" 435 a 705 c 659 g 458 t	PCLLPLSPPTADDRATAVATASRLØPYVLLBPBGGRAYQALHCPTGTEYTCKVYPVQ EAPAVLEPYARL PPHKHVARPTEVLAGTGULLYAFFTRTHGDMHGLVRSRHRI PEPERA VLFRQMATALAHCHQHGLVLRDLKLCRFVPADRBRKKLVLLENLEDSCVLTGPDDSLWD KHACPAYVGPEILSSRASYSGKAADVWSLGVALFFMLAGHFPFQDSBPVLLFGKIRRG	/codon_start=1 /proteIn_id="BAB15597.1" /proteIn_id="BAB15597.1" /db_xrefE"GI:10439924" /translation="MRATPLAAPAGSLSRKKRLBLDDNLDTERPVQKRARSGPQPRLP	/clone_lib="HBP" /note="cloning vector pME18SPL3" 2951371 /note="unnamed protein product"	/db_xref="taxon:9606" /clone="HEP10334" /cell_tine="HepG2" /cell_type="hepatoma"		construction, 5'- & 3'-end one pass sequencing: Departent of Virology and Human Genome Center, Institute of Medical Science, University of Tokyo (partly supported by Science and Technology Agency).	Fax:81-3-549-5416) NEDO human cDNA sequencing project supported by Ministry of International Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology; cDNA library	Submitted (29-AUG-2000) Sumio Sugano, Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure Analysis, Human Genome Center; Shirokane-dai, 46-1, Minato-ku, Tokyo 108-8639, Japan (B-mail:cdnal@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286,	2 (bases 1 to 2257) Sugano,S., Suzuki,Y., Ota,T., Obayashi,M., Nishi,T., Isogai,T., Shibahara,T., Tanaka,T. and Nakamura,Y. Direct Submission	Okamoto,S., Okitani,R., Ota,T., Suzuki,Y., Obayashi,M., Nishi,T., Shibahara,T., Tanaka,T., Nakamura,Y., Isogai,T. and Sugano,S. NEDO human cDNA sequencing project Unpublished	1 (altea) 1 (altea) 1 (altea) 1 (altea)	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Protein phosphatase and kinase proteins
Patent: WO 0120004-A 16 22-MAR-2001;
Incyte Genomics, Inc. (US)
Location/Qualifiers
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Homo sapiens
Bukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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Best Local Similarity 99.9%;
Matches 1992; Conservative
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Mammalia; Eutheria; Primates;
1 (bases 1 to 2488)
Shan,Y.X. and Yu,L.
Direct Submission
Submitted (03-MAR-2003) School
Genetics, Fudan University, He
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1680	CCAAGCCCAGCTCACTCTGGGAACTGTGTTCCCCAGCATCTCTGTCCTCTTGATT	1621	ફ
2112	CCTTTTCAGAGGAAAGGGAGCTATCCCTGTGCCAAAGGCTCCAGGCCTCTCCCCTGCAACT		망
1620	рададаладода от тестото селаладост с с посте с с с с с с с с с с с с с с с с с с	1561	ફ
2052	GGCACCTCTGTCCAAGGACAATCCCTTTCACAAACAAACCAGCTGCCTTTTGTATCTTGTA	1993	밁
1560	CACCTCTGTCCAAGGACAATCCCTTTCACAAACAAACCAGCTGCCTTTGTATCTTGTA	1501	१
1992	<i>p</i> -	1933	8
1500	TCACTGTCTACACTGGGTACACTTTGTACCAGTGTCGGCCTCCACTGATGCTGGTGCTCA	4	ई
1932	TGCTCACAGAGATGACAAACTGGCATCCTTGAGCTGACAACACTTTTCCATGACCATAGG	8	문
1440	TGCTCACAGAGATGACAAACTGGCATCCTTGAGCTGACAACACTTTTCCATGACCATAGG	u	ई
1872	GTGCCAAGCCCTGTTCTCGGTGCTGGGAGTACAGCAGTGAGCAAAGGAGACAATATTCCC	0	밁
1380	CCAAGC	w	१
1812	TGCTGTGTACACATCTGCTTTGTTCCACACACACAGTTCCTGCTTGGGTGCTTATCAG	1753	밁
1320	TGCTGTGTAC	N	ई
1752	AACTGAGCCAAACCTTCAGTGCCTTCCAGAAGGGAAAAGGCAGAAAGCCTGTGTGGAGTG	1693	밁
1260	AACTGAGCCAAACCTTCAGTGCCTTCCAGAAGGGAGAAAGGCAGAAGCCCTGTGTGGAGTG	201	१
1692	GCTCAGCTGCCAACAGTGGATTGAGTTTGGGGGTAGCTCCAAGCCTTCTCCTGCCTCTG	1633	문
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1632	GCCAGGGAAGAGGGAGACAGAGAAGTGGTTCTGTATGGCTAGGACCACCCTACTACA	573	망
	GCCAGGGAAGAGAGAGAGAGAGAGAGTGGTTCTGTATGGCTAGGACCACCCTACTACA	80	ঠ
1572	ACCCGATCCCATCTCTGGGAGGCTGCCCAGGTGGTCCCTGATGGACTGGGCTGGACGAA	513	당
	ACCCGATCCCATCTCTGGGAGGCTGCCCAGGTGGTCCCTGATGGACTGGGCTGGACGGAA	02	ঠ
1512	ACAGCCACAGGCATCCTGCACCCCTGGCTGCGACAGGACCCGATGCCCTTAGCCCCA	5	문
5	ACAGCCACAGGCATCCTCCTGCACCCCTGGCTGCGACAGGACCCGATGCCCCTTAGCCCCA	6	ई
1452	TCGGCCCCTGCCCGCTGTCTGGGTTCGCTGCCTTCGTCGGGAGCCAGCTGAACGGCTC	φ	망
960	TCGGCCCCTGCCGCTGTCTGGTTCGCTTGCTTCGTCGGGAGCCAGCTGAACGGCTC		ई
1392	GAGCCTGTCCTGCTCTTCGGCAAGATCCGCCGCGGGGCCTACGCCTTGCCTGCAGGCCTC	ω	6
900	GGCAAGATCCGCCGCGGGGCCTACGCCTTGCCTGCAGGCCT	841	ঠ
1332	GTGGCGCTCTTCACCATGCTGGCCGGCCACTACCCCTTCCAGG	1273	밁
840	TGGAGCCTGGGCGTGTCTTCACCATGCTGGCCGCCACTACCCCTTCCAGGACTCG	781	ঠ
1272	TACGTGGGACCTGAGATACTCAGCTCACGGGCCTCATACTCGGGCAAGGCAGCCGATGTC	1213	밁
780	ACGTGGGACCTGAGATACTCAGCTCACGGGCCTCATACTCGGGCAAGGCAGCCGATGT	721	ફ
1212	ACAAGCACGCGTGCCCAGC	1153	8
720	CTCCTGCGTGCTGACTGGGCCAGATGATTCCCTGTGGGACAAGCACGCGTGCCCAG	661	१
1152	CTGGA	1093	8
660	CTGTGTCGCTTTGTCTTCGCTGACCGTGAGAGAGAGAAGCTGGTGCTGGAGAACCTGGAG	601	8

	COMMENT	TITLE JOURNAL	REFERENCE	VERSION VERSION KEYWORDS SOURCE ORGANISM		RESULT 6 HS1103G7 LOCUS DEFINITION	Db 24	Qy 15	Db 24		, μ	Db 22	0y 18	N	L	N 1	Qy 16
During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP, Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C elegans/wormpep This sequence is follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. This sequence was generated from part of bacterial clone contigs of human chromosome 20, constructed by the Sanger Centre Chromosome 20 Mapping Group. Parther information can RPS-1103G7 is from the library RPC1-5 constructed by the group of Pieter de Jong, For further details see	requests clonerequest@sanger.ac.uk On Mar 19, 2000 this sequence version replaced gi:5541861.	Direct Submission Submitted (05-FEB-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA ITY R-mail emmiries hummisry@sanger ac uk Clone	<pre>BURATYOCA; Metazoa; Choroata; Craniata; vertebrata; Buteleostomi; Mammalla; Butheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 153170) Blacks</pre>	AL034548.25 GI:7263904 HTG; CpG island; NIPK; protein kinase; SOX22; SRY; VMP. Homo sapiens (human) Homo sapiens	similar to mouse WP, the gene for a novel protein kinase domains containing protein similar to phosphoprotein C8FW and rat NIPK, and the SOX22 gene for SRY (sex-determining region Y)-box 22. Contains five CpG islands, ESTs, STSs and GSSs, complete sequence.		473 GATTATGAAATAA 2486	981 GAATTATGAAATAA 1994	GTCCATACTCTAGGTTTTGGATACCATGAGTATGTTATGTTTACCTGTGCCTAATAAAGGA 2	353 GGCCACTIGGAAAAGICCCAGGIGGGACIGTICTICTIGGGGAACACTICGGGGICCACAATCCCAG 2412 921 GTCCATACTCTAGGTTTTTGGATACCATGAGTATGTTATGTTTACCTTTGTGTCTTAATAAAGGA 1980	GGCCACCTGGAAAGTCCCAGGTGGGACTCTTCTGGGGACACTTGGGGTCCACAATCCCAG	293 ATGGGGCTTCTGACCTGAGCACCAAGGTTGAGGGACAGGATTAGGCAGGGTCTGTCCTGT 2352	801 ATGGGGCTTCTGACCTGAGCACCAAGGTTGAGGGACAGGATTAGGCAGGGTCTGTCCTGT 1860	TGAGGCTAGTTCTTGTCTAACTCAAGACTGTTCTGGAATGAGGGTCCAGGCCTGTCAAC		AAGAGATTCTCCTTCCAGGCCTAAGCCTGGGATTTGGGCCAGAGATAAGAATCCAAACTA 223	681 AAGAGATTCTCCTTCCAGGCCTAAGCCTGGGATTTGGGCCAGAGATAAGAATCCAAACTA 1740

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                                                                                                                                                                                                                                              /note="30 copies 2 mer ca 88% conserved" 6710. .6824
        /note="match: GSS: Em:AQ701808"
7862. .8140
                                             complement (7590.
                                                                                                     7419. .7569
/note="AluSg/x repeat: matches 148.
                                                                                                                                    7126. .7415
/note="LlMA4A repeat: matches 5619.
                                                                                                                                                                                                                          note="MER50 repeat:
                                                                note="match: GSS: Em:AQ180303"
                                                                                                                                                                                  note="AluSx repeat: matches 7. .306 of consensus"
                                                                                                                                                                                                                                                                                                                           5798. .5865
/note="34 copies 2 mer aa 66% conserved"
5056. .6643
                                                                                                                                                                                                                                                                                                                                                                                                                                               note≡"L1MD2 repeat: matches 5684. .5861 of consensus"
5201. .5501
                                                                                                                                                                                                                                                                                                    note="MER67C repeat: matches 122. .710 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                         note="AluSx repeat: matches 1. .307 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note="MSTA repeat:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note="20 copies 2 mer aa 85% conserved"
complement(join(2194. .2243,126792. .126871))
note="match: GSS: Em:AQ377604"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'note="L1MA9 repeat: matches 6221. .6271 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       310. .4608
note="LIMD2 repeat: matches 5861. .6167 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              811. .4126
note="AluSx repeat: matches 1. .312 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note="MLT1H repeat: matches 115. .298 of consensus" complement(join(2146. .2243,126791. .126834)) note="match: GSS: Em:B59651"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note="match: STS: Em:266755" 734. .1888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note="THE1C repeat: matches 1.
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clone="RP5-1103G7"
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|mol_type="genomic DNA"
|db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note="MLT1H repeat: matches 387.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note="22 copies 2 mer ag 79% conserved"
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9. .129
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note="L1MD2 repeat: matches 5451. .5684 of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       matches 1. .424 of consensus"
                                                                                                                                                                                                                          matches 10.
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                                                                                                                                                                                      /note="LIM1 repeat: matches -1389. .-790 of consensus"
18158. .18195
/note="19 copies 2 mer tg 97% conserved"
18197. .18230
/note="AluSg/x repeat: matches 165. .197 of consensus"
18231. .18823
/note="MER52A repeat: matches 1. .672 of consensus"
complement (18827. .19180)
/note="match: 6853: Em:AQ599398"
19689. .1998
/note="MaluSg repeat: matches 1. .309 of consensus"
/note="match: 685: Em:AQ599398"
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/note="match: GSS: Em:AQ746749"
8019. .8151
/note="match: GSS: Em:AQ617736"
8152. .8316
/note="MER4B repeat: matches 416. .574 of consensus"
8349. .8643
/note="MER4D repeat: matches 362. .689 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="33 copies 2 mer at 68% conserved"
|11681. |11742
|/note="31 copies 2 mer ta 71% conserved"
|13519...13972
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/note="AluY repeat: matches 1. .299 of consensus"
8943. .9113
                                                                                                 note="MLT1J repeat: matches 255. .318 of consensus"
0592. .20756
                                                                                                                                         'note="AluSx repeat: matches 2.
10552. .20609
                                                                                                                                                                              0287. .20543
                                                                                                                                                                                                                                                                                                                                                                                                                      note="LIME rong | 7587. .18157
                                                                                                                                                                                                                                                                                                                                                                                                                                                            note="L1MA10 repeat: matches 6196. .6318 of consensus" 7155. .17587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note="Aluy repeat: matches 1. .302 of consensus"
.6895. .17021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="L1ME repeat: matches 5893. .5933 of consensus"
16595. .16894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Inote="LIME1 repeat: matches 5615. .5910 of consens

15873. .16174

Inote="AluSp repeat: matches 16. .313 of consensus"

16175. .16382

Inote="ILME1 repeat: matches 5400. .5615 of consensus"
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note="L1MB4 repeat: matches 5775. .5862 of consensus"
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note="MER1B repeat: matches 1. .337 of consensus"
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                                                                          e="MLT18 repeat: matches
                                   e="LlPBa repeat: matches -1128. .-1008 of consensus"
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repeat: matches -1537. .-1377 of consensus"
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                                                                            256. .421 of consensus"
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                                                 TCACAGAGATGACAAACTGGCATCCTTGAGCTGACAACACTTTTCCATGACCATAGGTCA
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/note="LIMA7 repeat: matches 5864 .5945
21280 .21627
/note="L2 repeat: matches 2250 .2617 of
21628 .21884
/note="match: GSS: Em:B41180"
21628 .21744
/note="match: GSS: Em:AQ058160"
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Best Local Similarity 99.8%;
Matches 1075; Conservative
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            109 TTGGATGACAACTTAGATACCGAGCGTCCCGTCCAGAAACGAGCTCGAAGTGGGCCCCAG
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Novel human protein kinases and protein kinase-like Patent: WO 0138503-A 9 31-MAY-2001;
Sugen, Inc. (US)
                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                              ATGCGAGCCACCCCTCTGGCTGCTCCTGCGGGTTCCCTGTCCAGGAAGAAGCGGTTGGAG
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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                                                               CCCTTAGCCCCAACCCGATCCCATCTCTGGGAGGCTGCCCAGGTGGTCCCTGATGGACTG
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                                             GGGCTGGACGAAGCCAGGGAAGAGGAGGAGGACAGAGAAGTGGTTCTGTATGGCTAG
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Matches 1073; Conservative
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Homo sapiens
Sukaryota, Metazoa; (
Mammalia; Eutheria; I
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Mammalian tribbles signaling pathway.
Mammalian thereto
Patent: WO 02053743-A 3 11-JUL-2002;
Interleukin Genetics, Inc. (US)
Location/Qualifiers
            GTGCTGGAGAACCTGGAGGACTCCTGCGTGCTGACTGGGCCAGATGATTCCCTGTGGGAC
                                                                                                                                                                        GTGCTCTTCCGCCAGATGGCCACCGCCCTGGCGCACTGTCACCAGCACGGTCTGGTCCTG
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AAGCACGCGTGCCCAGCCTACGTGGGACCTGAGATACTCAGCTCACGGGCCTCATACTCG
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a 374 c 327 g 20
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Pred. No. 9.6e-193;
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1123 TAG 1125	49 ATGCGAGCCACCCCTCTGGCTGCTCCTGCGGGTTCCCTGTCCAGGAAGAAGCGGTTGGAG 10	ş
1063 GGACTGGGGCTGGACGAAGCCAGGGAAGAGGGAGGGAGACAGAGAAGTGGTTCTGTATGGC 	Query Match 51.2%; Score 1054.6; DB 9; Length 1083; Oy Best Local Similarity 99.1%; Pred. No. 9.6e-193; Db Matches 1073; Conservative 0; Mismatches 4; Indels 6; Gaps 1;	Query Best Matcl
1003 CCGATGCCCTTAGCCCCAACCCGATCCCATCTCTGGGAGGCTGCCCAGGTGGTCCCTGAT	OUNT 176 a	BASE CO
943 GAGCCAGCTGAACGGCTCACAGCCACAGGCATCCTCCTGCACCCCTGGCTGCGACAGGAC	PCLLPLSPPTAPDRATAVATASRLGPYVLLBPBEGGRAYQALHCPTGTBYTCKVYPVQ EALAVLBPYARVPPHKIVARPTEVLAGYQLLYAPTRTHGDMISLVRSHRI PBPBAA VLPRQMATALAHCHQHGLVLRDLKLCRPVFADADDREKKKLVLENLBDSCVLTGPDDSL WDKHACPAYVGPEILSSRASYSGKAADVWSLGVALFTMLAGHYPPQDSSPVLLPGKIR	
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823 TACCCCTTCCAGGACTCGGAGCCTGTCCTGCTCTTCGGCAAGATCCGCCGCGGGCCTAC	/mol_type="mRNA"	Ω
763 GGCAAGGCAGCCGATGTCTGGAGCCTGGGCGTGGCGCTTCACCATGCTGGCCGGCC	EATURES Location/Qualifiers Qy BOURCE 11083 Db /organism="Homo sapiens" . Db	FEATUR
	,D.H., Qwarnstrom,E.E. and Dower,S.K. 00) Division of Molecular & Genetic Medicine, eld, Royal Hallamshire Hospital, Floor M,	AUTH TITLI JOURU
643 GTGCTGGAGAACCTGGAGGACTCCTGCGTGCTGACTGGGCCAGATGATTCCCTGTGGGAC		TITLI JOUR REPEREI
589 CGTGATCTCAAGCTGTGTCGCTTTGTCTTCGCTGACCGTGAGAGGAAGAAGCTG	100	REFERE!
529 GTGCTCTTCCGCCAGATGGCCACCGCCCTGGCGCACTGTCACCAGCACGGTCTGGTCCTG	NISM OS N	VERSION KEYWORDS SOURCE ORGANI
469 CATGGGGACATGCACAGCCTGGTGCGAAGCCGCCACCGTATCCCTGAGCCTGAGGCTGCC	AP250311 AP250311 1083 bp mRNA linear PRI 01-JUN-2001 OY DEPINITION Homo sapiens SKIP3 mRNA, complete cds. Db	AP250311 LOCUS DEPINITI ACCESSIO
409 GCTCGGCCCACTGAGGTCCTGGCTGGTACCCAGCTCCTCTACGCCTTTTTCACTCGGACC	1081 TÁG 1083 QY	RESULT
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229 GCTGTGGCCACTGCCCTCTTGGGCCCCTATGTCCTCCTGGAGCCCGAGGAGGGCGGGGGGGG	1001	\$ \$
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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     CGTGATCTCAAGCTGTCGCTTTGTCTTCGCTGACCGTGAGAGGAAGAAGCTGGTGCTG
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                                                                                                                                                                          GCTCGGCCCACTGAGGTCCTGGCTGGTACCCAGCTCTCTACGCCTTTTTTCACTCGGACC
                                                                                                                                                                                                                                   GTCCAGGAAGCCCTGGCCGTGCTGGAGCCCTACGCGCGGGCTGCCCCCCGCACAAGCATGTG
                                                                                                                                                                                                                                                                        CGGGCCTACCAGGCCCTGCACTGCCCTACAGGCACTGAGTATACCTGCAAGGTGTACCCC
                                                                                                                                                                                                                                                                                         CGGGCCTACCGGGCCCTGCACTGCCCCTACAGGCACTGAGTATACCTGCAAGGTGTACCCC
                                                                                                                                                                                                                                                                                                                              GCTGTGGCCACTGCCTCCCGTCTTGGGCCCCTATGTCCTCCTGGAGCCCGAGGAGGGCGGG
                                                                                                                                                                                                                                                                                                                                                GCTGTGGCCACTGCCTCCCGTCTTGGGCCCTATGTCCTCCTGGAGCCCGAGGAGGAGGGCGGG
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1329 c 294 g 182 t
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Pred. No. 3.6e-144;
0; Mismatches 28;
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Kiss-Toth,E., Dempsey,C., Jozs
Bagstaff,S.M., Wyllie,D.H., Ha
Qwarnstrom,B.B. and Dower,S.K.
Direct Submission
                                                                                                                                                                                                                                                                                            Kiss-Toth, B., Dempsey, C., Jozsa, V., Caunt, Bagstaff, S.M., Wyllie, D.H., Harte, M., O'Ne Qwarnstrom, E.E. and Dower, S.K. Mammalian homologs of Drosophila tribbles activated protein kinase signaling
                                                                                                                                                    Submitted (12-MAR-2001) Division of Genomic Medicine, University Sheffield, Royal Hallamshire Hospital, Floor M, Glossop Road, Sheffield S10-2JF, UK
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AF358868
Mus musculus TRB-3 mRNA,
AF358868
                                                                                                                                                                                                                                                                                Unpublished
                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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182. .1246
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                                                                                                               TACTCAGCTCCCGGCCATCCTACTCTGGCAAAGCGGCTGATGTCT
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                    TCGGCAAGATCCGCCGCGGGGCCTACGCCTTGCCTGCAGGCCTCTCGGCCCTGCCCCT
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  TTGGCAAGATCCGTANAGGGACCTTTGCCCTGCCTGAGGGCCTATCAGCCCCAGCCCGCT
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GLERQMASAVAHCHKHGLVLRDLKLRE PVFSNCERTKLYELENLEDACVHTGSDDSHD
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TPALPEGLSAPARCLI RCLLRKEPSERLVALGI LLHPWLREDHGRVS PPQSDRREMDQ
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Sequence
AX364906
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Novel nucleic acid and amino acid sequences
Patent: WO 0206315-A 57 24-JAN-2002;
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Similarity 98.2%;
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GAGGTCCTGGCTGGTACCCAGCTCCTACGCCTTTTTCACTCGGACCCATGGGGACATG
                   GAGGTCCTGGCTACCCAGCTCCTCTACGCCTTTTTCACTCGGACCCATGGGGACATG
                                                                   CTGGCCGTGCTGGAGCCCTACGCGCGGCTGCCCCCGCACAAGCATGTGGCTCGGCCCACT
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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3; Mismatches 6;
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Sequence 72
AX364921
AX364921.1
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Novel nucleic acid and amino acid sequences
Patent: WO 0206315-A 72 24-JAN-2002;
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Mammalia, Eutheria, Primates,
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Matsuda,K.M., Kojima,S. and Nakayama,T.

Matsuda,K.M., Kojima,S. and Nakayama,T.

Direct Submission
Submitted (09-DEC-1998) Keiko Mayumi Matsuda, SHIONOGI and Co.

Itd., Shionogi Institute for Medical Science; 2-5-1 Mishima,

Settsu-shi, Osaka 566-0022, Japan
(B-mail:keiko.matsuda@shionogi.co.jp, Tel:81-6-6382-2612(ex.465),
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99262087
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Mammalia; Eutheria;
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                           /tranalation="Maatslaasadvecrkkeleeddnidvecevlkryrdeeedety
Psippasdlspavapatrigpyillereggnctyralhcetgteytckvypaseagav
Lapyarlethghvaretsvilgsqllyteftkthgdlhslvrsergibeseagalerq
Masavahchegglilreklrretvesncertkulenlebacvmtgeddsluddhale
Ayvgeeilssresysgraadvmslgvaletmlagryppodseallegktrrgtpale
Egisasarciircilrrepserlvalgillhpwlredcsqvspprsdrremdqvvpdg
                                                                                                                       /codon_start=1
/product="kinase"
/protein_id="BAA77582.1"
/db_xref="GI:4827159"
                                                                                                                                                                                                                                                                                   /db xref="taxon:10118"
/ceIl_line="PC12"
/cell_type="pheochromocytoma"
                                                                                                                                                                                                                         /gene="NIPK"
                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                        /note="neuronal cell death inducible (NIPK); induced by NGF-depletion"
                                                                                                                                                                                                                                                         gene="NIPK"
                                                                                                                                                                                                                                                                                                                                       organism="Rattus sp.
mol_type="mRNA"
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Rodentia;
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Sciurognathi; Muridae
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Best Local Similarity
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                 GTCTGGTTCGCTGCCTTCGTCGGGAGCCAGCTGAACGGCTCACAGGCACAGGCATCC
                                                               TCGGCAAGATCCGCCGCGGGGCCTACGCCTTGCCTGCAGGCCTCTCGGCCCCTGCCCGCT
                                                                                                   CGCTCTTCACCATGCTGGCTGGCCGATACCCGTTCCAGGACTCTGAACCAGCCCTGCTCT
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GCCTCATCCGCTGTCTCCGCAGGGAGCCTTCAGAGCGACTTGTGGCCCTGGGAATCC
                                                  TTGGCAAGATCCGTAGAGGGACCTTTGCCCCTGCCTGAGGGCCTATCAGCCTCTGCTCGAT
                                                                                                                      CGCTCTTCACCATGCTGGCCGGCCACTACCCCCTTCCAGGACTCGGAGCCTGTCCTGCTCT
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/note="27 a nucleotides"
/note="27 a nucleotides"
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Pred. No. 2.9e-110;
D; Mismatches 311;
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COMMENT
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AUTHORS
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Riausner, R.D., Collins, P.S., Wagner, L., Schemmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetcw, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, P.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Villalon, D.K., Muzny, D.M., Madan, A., Rodrigues, S.,
Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Boutfard, G.G., Blakesley, R. W., Touchman, J.W., Green, B.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and mouse cDNA sequences
AL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.B. Consortium of DNA Sequencing by: Baylor College of Medicine Human Sequencing Conter
                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission

Direct Submission

Submitted (20-AUG-2001) National Institutes of Health, Mammalian Submitted (20-AUG-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 (bases 1 to
Strausberg, R.
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BC012955 CT. COMPLETE COMPANY CO
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Mammalia; Butheria; Rodentia;
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This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, Similarity but not identity to protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, &
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny,
A.N., Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCGCCCGGGCCCACGCGGAACGACGGGGGGGGAGATGCGAGCCACCCCTCTGGCTGCTCCTG
               CAGGCACTGAGTATACCTGCAAGGTGTACCCCCGTCCAGGAAGCCCTGGCCGTGCTGGAGC
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/product="TIB-3"
/protein_id="AHI2955.1"
/protein_id="AHI2955.1"
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/db_xref="GI:15277945"
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/db_xref="CountD1:228775"
/db_xref="CountD1:228775"
/db_xref="CountD1:228775"
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/translation="MRATPLAASADVSCRKKPLEFDDNIDAKCPVTKRVREPEPPAS
PSILLPPSPPASDLSPANAPATRLGPYILLEREROGSCSYRALHCPTGYTRSTRGIPEPPAS
EAQAVLAPYARLPTHQHVARPTEVLLGSRFLYIFPTKTHCDLHSLVRSRRGIPEPPAA
ELAQAVLAPYARLPTHQHVARPTEVLLGRIFTSNCERTKLVLENLEBACCWTGSDDSLMD
KHACPAYVGPBILSSNPSYSBPVLLFGKIRRGTFALPEGLSAPARCLIRCLLRKEPSE
RLVALGILLHPMLREDHGRVSPPQSDRREMDQVVPDGPQLEEAEEGEVGLYG"
13 a 560 c 572 g 424 t
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/db_xref="LocusID:228775"
/db_xref="MGI:1345675"
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/clone="MGC:18731 IMAGE:3980838"
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/strain="PVB/N"
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	1991 АТААЛЛАЛАЛАЛАЛАЛАЛАЛАЛАЛАЛАЛАЛАЛАЛА 2026 	
1990	1932 AGGTTTTGGATACCATGAGTATGTATGTTTA-CCTGTGCCTAATAAAGGAGAATTATGAA 1990 	
1931 1873	1872 AAGTCCCAGGTGGGACTCTTCTGGGGACACTTGGGGTCCACAATCCCAGGTCGATACTCT 1931	
1871 1817	1813 ACCTGAGCACCAAGGTTG-AGGGACAGGATTAGGCAGGTCTGTCCTGTGGCCACCTGGA 1871 	
1812 1759	1754 TGTCTAACTCAAGACTGTTCTGGAATGAGGGTCCAGGCCTGTCAACCATGG-GGCTTCTG	
1753 1703	1694 TCCAGGCCTAAGCCTGGGATTIGGGCCAGAGATAAGAATCCAAACTATGAGGCTAGTTCT 1753	
1693 1648	1634 CAGCTCACTCTGGGAACTGTGTTCCCAGCATCTCTGTCCTCTTGATTAAGAGATTCTCCT 1693	
1633	1577 GAGGTATCCCTGTGCCAAAGGCTCCAGGCCTCTCCCCTGCAACTCAGGACCCAAGCC	
1576 1539	1517 GACAATCCCTTTCACAAACAAACCAGCTGCCTTTGTATCTTGTACCTTTTCAGAGAAAGG	
1483	1440 GCACGTTTCCTACC-GGGGCTGTCTTCTCTGGTGCTGGTTCATGG 1483	

Search completed: January 16, 2004, 14:49:00 Job time: 7734.16 secs

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14.8	14.8	14.8	14.9	14.9	14.9	15.0		15.0	15.0	15.0	15.0	15.0	15.1	15.2	15.3	15.3	15.4	15.5	15.6	15.7	15.7	15.7	15.7	15.7	15.8	16.0	16.2	16.6
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ALIGNMENTS

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RESULT 1

OBKO17

OBKO17

PRELIMINARY; PRT; 343 AA.

AC Q8KO17; PRT; PRT; PRT; PRT; PRT; PRT; PRT;

DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)

DE TRB2 (CSFW ORF protein homolog).

OC MARMARIA; Extensional; Publetia; Sciurognathi; Muridae; Mus.

OC MARMARIA; BC10000; Extensional and Proteina; PROTEIN ARCHAPAT; BAC1002) to the EMBL/GenBank/DDBJ databases.

RC TISSUB-Kidney;

RL SEQUENCE PROM N.A.

RE SEQUENCE PROM N.A.

RC STRAIN-C57BL/63; TISSUB-Aorta and vein, Cerebellum, and Retina;

RC STRAIN-C57BL/63; TISSUB-AORTA and vein,
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                                             wilkin F., Suarez-Huerta N., Robaye B., Peetermans J.,
Dumont J.E., Maenhaut C.,
"Characterization of a phosphoprotein whose mRNA is rec
mitogenic pathways in dog thyroid cells.";
Eur. J. Biochem. 248:660-669(1997).
EMBL; X99144; CAA67581.1; -.
EMBL; X99144; CAA67581.1; -.
HSSP; Q63450; 1A06.
InterPro; IPR000719; Prot kinase.
Pfam; PF00069; pkinase; 1.
ProDom; PD000001; Prot kinase; 1.
ProDom; PD000001; Prot kinase; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
ATP-binding; Transferase.
SEQUENCE 343 AA; 38786 MW; BF8D1300DACB84FA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Thyroid;
TISSUE=Thyroid;
MEDLINE=97067069; PubMed=8910471;
MEDLINE=97067069; PubMed=8910471;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Canis familiaris (Dog).
Bukaryota; Metazoa; Chordata; C
Mammalia; Butheria; Carnivora;
MCBI_TaxID=9615;
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01-NOV-1996 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                           "Identification and Characterization of Novel Genes Modulated in Thyroid of Dogs Treated with Methimazole and Propylthiouracil."; J. Biol. Chem. 271:28451-28457(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CSFW ORF protein.
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MEDLINE=98000262; PubMed=9342215;
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Pred. No. 1.8e-55;
 Score 754.5; DB 6;
Pred. No. 2.4e-55;
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EMBL; D07119; BAA13250.1; -.
EMBL; BC002637; AAH02637.1; -.
HSSP; Q63450; 1A06.
InterPro; IPR000719; Prot_kinase.
Pfam; PP00069; pkinase; 1.
ProDom; PD000001; Prot_kinase; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1
ATP-binding; Transferase.
SEQUENCE 343 AA; 38800 MW; BF8B73661
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Q92519;
O1-FRB-1997 (TTEMBLrel. 0:
O1-FRB-1997 (TTEMBLrel. 0:
O1-MAR-2003 (TTEMBLrel. 2:
GS3955 (GS3955 protein).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human)
Bukaryota; Metazoa;
Mammalia; Eutheria;
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HVARPTEVLAGTQLLYAPFTRTHGDMHSLVRSRHRIPBPEAAVLFRQMATALAHCHQHGL
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Primates;
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activated protein kinase signaling,";
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ dat
EMBL; AF358667; AAM45477.1; -.
Interpro; IPR000719; Prot kinase.
Interpro; IPR0012290; Ser_thr_pkinase.
Interpro; IPR001245; Tyr_pkinase.
Interpro; IPR001245; Tyr_pkinase.
Pfam; PP00069; pkinase; 2.
ProDom; PD000001; Prot kinase; 1.
SMART; SM00220; S_TKC; 1.
SMART; SM00219; TyrKC; 1.
SMART; SM00219; TyrKC; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
ATP-binding; Transferase.
SEQUENCE 343 AA; 38758 MW; 0839658882087D74 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-2002
01-OCT-2002
01-MAR-2003
TRB-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kiss-Toth E., Dempsey
Bagstaff S.M., Wyllie
Dower S.K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata,
Mammalia, Eutheria, Rodentia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Mammalian homologs of Drosophila tribbles (htrb)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         163;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                    HVARPTEVLAGTQLLYAFFTRTHGDMHSLVRSRHRIPBPBBAAVLFRQMATALAHCHQHGL
  EPAERLTATGILLHPWLRQDPMPLAPTRSHLWEAAQVVPDGLGLDEAREB
                                                                                                               GKAADVWSLGVALFTMLAGHYPPQDSEPVLLFGKIRRGAYALPAGLSAPARCLVRCLLRR
                                                                                                                                                                                                 VLRDLKLCRFVFADRERKKLVLENLEDSCVLTGPDDSLWDKHACPAYVGPBILSSRASYS
                                                                                                                                                                                                                                                                 NINQITBILLGETKAYVFFERSYGDMHSFVRTCKKLREEBAARLFYQIASAVAHCHDGGL
                                                                            GKAADVWSLGVMVYTMLVGRYPPHDIEPSSLFSKIRRGQPNIPETLSPKAKCLIRSILRR
                                                                                                                                                                        VLRDLKLRKFIFKDEERTRVKLESLEDAYILRGDDDSLSDKHGCPAYVSPEILNTSGSYS
                                                                                                                                                                                                                                                                                                                                                                V---SCIGKYLLLEPLEGDHVFRAVHLHSGEELVCKVFEISCYQESLA---PCFCLSAHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RATPLAAPAGSLSRKKRLELDDNLDTERPVOKRARSGPOPRLPPCLLPLSPPTAPDRATA
                                                                                                                                                                                                                                                                                                                                                                                                               VATASRLGPYVLLEPEEGGRAYRALHCPTGTEYTCKVYPV---QEALAVLEPYARLPPHK
                                                                                                                                                                                                                                                                                                                                                                                                                                                              RSTPITIARYGRSRNKTQDFEE-LSSIRSAB-----PSQSFSPNLGSPSPPETPNLSHC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EPAERLTATGILLHPWLRQDPMPLAPTRSHLWEAAQVVPDGLGLDEAREBEGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GKAADVWSLGVMLYTMLVGRYPFHDIBPSSLFSKIRRGQFNIPETLSPKAKCLIRSILRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GKAADVWSLGVALFTMLAGHYPFQDSEPVLLFGKIRRGAYALPAGLSAPARCLVRCLLRR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EPSERLTSQEILDHPWFSTD-----FSVSNSAYGAKEVSDQLVPDVNMEENLD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        38758 MW; 0B3965B8B2087D74 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                39.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Jozsa V., Cu., Harte M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 753; DB 11;
Pred. No. 3.1e-55;
9; Mismatches 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Caunt J.,
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L.A.J., Qwa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 343;
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RESULT
Q96RU8
AC Q9
DT 01
DT 01
DT 01
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DT 01
CS HC
OC BU
OC Ma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local S
Matches 163
                                                                                           Q96RU8;
Q96RU8;
01-DEC-2001
01-DEC-2001
01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9EQL6
Q9EQL6;
Q1-MAR-2001
01-MAR-2001
01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NON TER
SEQUENCE
Homo sapiens (Human)
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                          SKIP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      receptor-induced gene.";
Submitted (NOV-1999) to the
EMBL; AF205438; AAG35664.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00069; pkinase; 1.
ProDom; PD000001; Prot_kinase; 1.
PROSITS; PS50011; PROTEIN_KINASE_DOM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nitsch R.M., "Identification of a novel nuclear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-Sprague-Dawley, TISSUE-Brain, Mayhaus M., von der Kammer H., Klaudiny
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa,
Mammalia, Butheria,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TP-binding; Receptor; Transferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR000719; Prot_kinase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 166 MATALAHCHOHGLVI.RDLKI.CRFVFADRERKKI.VI.BNI.EDSCVI.TGPDDSIMDKHACPAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      122
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                                                                                                                                                                                                                                                                                                           PKARCLIRSLLRREPSERLTAPEILLHPWFEYVLEP-GYVDSEVGTSDQIVPE
                                                                                                                                                                                                                                                                                                                                                        APARCLVRCLLRRBPAERLTATGILLHPWLRQDPMPLAPTRSHLWEAAQVVPD
                                                                                                                                                                                                                                                                                                                                                                                                       VSPBILNTTGTYSGKAADVWSLGVMLYTLLVGRYPFHDSDPSALFSKIRRGQFCIPEHVS
                                                                                                                                                                                                                                                                                                                                                                                                                              VGPEILSSRASYSGKAADVWSLGVALFTMLAGHYPFQDSBPVLLFGKIRRGAYALPAGLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IVSAVAHCHOSAIVLGDLKLRKFVFSTEERTQLRLESLEDTHMIKGEDDALSDKHGCPAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DKIRPYTQLPSHRNITGIVEVILGESKAYVFFEKDFGDMHSYVRSRKRLREEBAARLFKQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AVLEPYARLPPHKHVARPTEVLAGTQLLYAFFTRTHGDMHSLVRSRHRIPBPEAAVLFRQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RATPLAAPAGSLSRKKRLELDDNLDTERPVQKRARSGPQPRLPPCLLP---LSPPTAP--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EPSERLTSQEILDHPWFSTD------PSVSNSGPGAKEACDQ 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POPPPSAQGTGGSCVSAPGPSRIADYLLLPLAEREHVSRALCIHTGRELRCKVFPIKHYQ 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----DRATAVATASRLGPYVILLEPEEGGRAYRALHCPTGTEYTCKVYPVQEAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RGPALLFPAARGTPAKRL----LDTDDAAAVAAKC---PRLSECSNPPDYLSPPGSPCS
                                                                                              (TrEMBLrel. (TrEMBLrel. (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     364 AA; 40377 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (TrEMBLrel. 16, Created)
(TrEMBLrel. 16, Last sequence update)
(TrEMBLrel. 23, Last annotation update)
oupled receptor induced protein GIG2 (Pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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  Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       39.6%; Score 749.5; DB 1
46.2%; Pred. No. 6.6e-55;
tive 46; Mismatches 119
                                                                                              19,
19,
23,
                                                                                           Created)
Last sequence up
Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL/GenBank/DDBJ
  Craniata; Ve
Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Craniata; Vertebrata; I
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
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  Vertebrata; Buteleostomi; i; Hominidae; Homo.
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on update)
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Best Local Similarity
Matches 162; Conser
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"Identification of pro-inflammatory cytokine signalling net
components by transcription expression screening.";

L Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; APZ50310; AAK58174.1; -.

R InterFro; IPR000719; Prot_Kinase.

R Pfam; PP00069; pkinase; 1.

R ProDom; PD000001; Prot_Kinase; 1.

R ProDom; PD000001; Prot_Kinase; 1.

R ProDom; PD000001; PROTEIN_KINASE_DOM; 1.

R PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.

SEQUENCE 372 AA; 40980 MM; 3EZB5C87A4F98FDB CRC64;
"Identification of a novel nuclear factor Gig2, as an mi receptor-induced gene.", submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases. EMBL, AP205437; AAG35663.1; -. InterPro; IPR000719; Prot_kinase. Pfam, PP00069; pkinase; 1. Problem; PD000001; Prot_kinase; 1. PROSITE; PS50011; PROTEIN_KINASE_DOM; 1. ATP-binding; Receptor; Transferase. SEQUENCE 372 AA; 41008 MW; 5F54E50924Bl365B CRC64;
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09H2Y8;
01H2Y8;
01-MAR-2001 (TrEMBLrel. 16,
01-MAR-2001 (TrEMBLrel. 23,
01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                Mayhaus M.,
                                                                                                                                                                                                                                                                                                                                              TISSUE=Kidney,
                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE PROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human)
Eukaryota, Metazoa,
Mammalia, Butheria,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A
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induced protein GIG2.
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Pred. No. 1.8e-54;
7; Mismatches 126;
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Best Local Similarity
                                                                                                                          the RIKEN Genome Exploration Research Group P
"Analysis of the mouse transcriptome based on
60,770 full-length cDNAs.";
Nature 420:563-573(2002).
EMBL; BC006800; AAH06800.1; -.
EMBL; AK028626; BAC26038.1; -.
InterPro; IPRO00719; Prot kinase.
Pfam; PF00069; pkinase; 1.
ProDom; PD000001; Prot kinase; 1.
PROSITE; PS50011; PROTEIN KINASE_DOM; 1.
ATP-binding; Transferase.
SEQUENCE 372 AA; 41281 MW; AD29BB4E640B4B
                                                                                                                                                                                                                                                                                                                                                                                                                              Q91W04;
Q91W04;
Q1-DBC-2001 (TrEMBLrel. 19;
Q1-DBC-2001 (TrEMBLrel. 23;
Q1-MAR-2003 (TrEMBLrel. 23;
Q1-MAR-2003 (TrEMBLrel. 23;
Q1-MAR-2003 (Mouse).
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordat
Mammalia; Eutheria; Rodenti
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                                                                                                                                                                                                                                                                                                                STRAIN=C57BL/6J;
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                                                                                         Similarity
                                        RATPLAAPAGSLSRKKRLELDDNLDTERPVQKRARSGPQPRLPPCLLP---LSPPTAP--
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(TTEMBLrel. 19, Last sequence update)
(TTEMBLrel. 23, Last amoutation update)
phosphoprotein regulated by mitogenic pathways.
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                                                                                                                                                                                                                                                                                                                                                                              tumor;
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Rodentia;
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Pred. No. 2.6e
46; Mismatches
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                                                                                        Score 742.5;
Pred. No. 2.
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                                                                                                                              AD29BB4E640B4B62 CRC64;
                                                                            Mismatches
                        -LDTD----DAGAVAAKCPRLSECSSPPDYLSPPGSPCS

    YVLLEPEEGGRAYRALHCPTGTBYTCKVYPVQEAL

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Best Local
Matches 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q8K4K4
Q8K4K4;
01-OCT-2002
01-OCT-2002
01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata;
Mammalia; Butheria; Rodentia;
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                    ProDom; PD000001; Prot_kinase; 1.
SMART; SM00220; S.TKC; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM;
ATP-binding; Transferase.
SEQUENCE 372 AA; 41282 MW; 3A3DE82
                                                                                                                                                                                                                                                                                                                                                                 activated protein kinase signaling.";
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ
EMBL; AP358866; AAM45478.1; -.
InterPro; IPR000719; Prot kinase.
InterPro; IPR002290; Ser thr pkinase.
Pfam; PP00069; pkinase; Z.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Dower S.K.,
"Mammalian homologs of Drosophila tribbles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Riss-Toth E., Dempsey Bagetaff S.M., Wyllie
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                                                             MATALAHCHOHGLVLRDLKLCREVEADRERKKLVLENLEDSCVLTGPDDSLWDKHACPAY
                                                                                              DKIRPYIQLPSHSNITGIVEVLLGESKAYVFFEKDFGDMHSYVRSRKKLREEEAARLFKQ
                 VGPEILSSRASYSGKAADVWSLGVALFTMLAGHYPFQDSEPVLLFGKIRRGAYALPAGLS
                                                                                                                       AVLEPYARLPPHKHVARPTEVLAGTQLLYAFFTRTHGDMHSLVRSRHRIPEPEAAVLFRQ 165
VSPBILNTTGTYSGKAADVWSLGVMLYTLWVGRYPPHDSDPSALPSKIRRGQPCIPEHVS
                                                                                                                                                POPPPSTQGTGGSCVSSPGPSRIADYLLLPLABREHVSRALCIHTGRELRCKEFPIKHYQ 128
                                                                                                                                                                                                                        RATPLAAPAGSLSRKKRLELDDNLDTERPVQKRARSGPQPRLPPCLLP---LSPPTAP--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MATALAHCHQHGLVLRDLKLCRFVFADRERKKLVLENLEDSCVLTGFDDSLWDKHACFAY
                                                                                                                                                                        -----Dratavatasrigp-----yvllepeeggrayralhcptgteytckvypvqeal
                                                                                                                                                                                                RGPGLLFPAARGTPAKRL-----LDTD---DAGAVAAKCPRLSECSSPPDYLSPPGSPCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PKARCLIRSLLRREPSERLTAPQILLHPWPEYVLEP-GYVDSEIGTSDQIVPE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VGPEILSSRASYSGKAADVWSLGVALFTMLAGHYPFQDSEPVLLFGKIRRGAYALPAGLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DKIRPYIQLPSHSNITGIVEVLLGESKAYVPPBKDFGDMHSYVRSRKRLREBEAARLFKQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AVLEPYARLPPHKHVARPTEVLAGTQLLYAPPTRTHGDMHSLVRSRHRIPBPEAAVLFRQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IVSAVAHCHOSAIVLGDLKLRKFVFSTEERTQLRLESLEDTHIIKGEDDALSDKHGCPAY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 (TrEMBLrel.
2 (TrEMBLrel.
3 (TrEMBLrel.
                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                   41282 MW; 3A3DE82B46CD907F CRC64;
                                                                                                                                                                                                                                                               38.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  D.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22,
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                                                                                                                                                                                                                                                   44;
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Last
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
                                                                                                                                                                                                                                                   Score 729.5; DB 1
Pred. No. 3.3e-53;
4; Mismatches 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence update)
annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   <u>=</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Caunt J., I., O'Neill
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                                                                                                                                                                                                                                                                           DB 11;
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                                                                                                                                                                                                                                                   121;
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L.A.J., Qwa
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                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                           Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Qwarnstrom
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REPRESON SON DEPT DE LE
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Best Local &
Matches 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Strausberg R.;
Submitted (ARR-2002) to the EMBL/GenBank/Di
EMBL; BC027159, AAH27159, 1; -.
InterPro; IPR000719; Prot kinase.
Pfam; PP00069; pkinase; 1.
ProDom; PD000001; Prot kinase; 1.
PROSITE; PS50011; PROTEIN KINASE DOM; 1.
Hypothetical protein; ATP-binding; Transfe.
NON TER
                                           Homo sapiens (Human).
Bukaryota, Metazoa, C
Mammalia, Butheria, P
NCBI_TaxID=9606;
                                                                                                                        O15180
O15180;
O1-JAN-1998
O1-JAN-1998
O1-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q8R2V8;
01-JUN-2002
01-JUN-2002
SEQUENCE FROM N.A. TISSUE=Thyroid; Wilkain F.;
                                                                                                           01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Phosphoprotein (Fragment).
                                                                                                   CBPW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical 29.2 kDa protein (Fragment).
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQÜENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q8R2V8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                         DDSLWDKHACPAYVGPEILSSRASYSGKAADVWSLGVALFTWLAGHYPFQDSBPVLLFGK
                                                                                                                                                                                                                                                               AQVVPDGLGLDEAREE 348
                                                                                                                                                                                                                                                                                                                                                                                                          RIPBPEAAVLFRQMATALAHCHQHGLVLRDLKLCRFVFADRERKKLVLENLEDSCVLTGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                           CKVYPV---QEALAVLEPYARLPPHKHVARPTEVLAGTQLLYAFFTRTHGDMHSLVRSRH
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                                                                                                                                                                                                                                                                                        IRRGQFNIPETLSPKAKCLIRSILRREPSERLTSQEILDHPWFSTD
                                                                                                                                                                                                                                                                                                                                                                                                                                             CKVFBISCYQESLA----PCFCLSAHSNINQITEILLGETKAYVFFBRSYGDMHSFVRTCK
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                                                                                                                                                                                                                                                                                                              IRRGAYALPAGLSAPARCLVRCLLRREPAERLTATGILLHPWLRQDPMPLAPTRSHLWEA
                                                                                                                                                                                                                                                                                                                                          DDSLSDKHGCPAYVSPEILNTSGSYSGKAADVWSLGVMLYTMLVGRYPFHDIEPSSLFSK
                                                                                                                                                                                                                                                                                                                                                                                           KLREBEAARLFYOIASAVAHCHDGGLVLRDLKLRKFIFKDEERTRVKLESLEDAYILRGD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 257 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34.5%;
llarity 52.3%;
Conservative 3
                                                                                                                                                                          PRELIMINARY;
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                                                           Chordata;
Primates;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 653; DB 11;
Pred. No. 5.7e-47;
4; Mismatches 68;
                                                          Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                          PRT;
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RP SEQUENCE FROM N.A.

RC STRAIN=BERKELEY;

RX MEDLINE=20196006; PubMed=10731132;

RX MEDLINE=20196006; PubMed=10731132;

RX Adams M.D., Ceiniker S.E., Holt R.A., Bvans C.A., Gocayne J.D.,

RA Adams M.D., Ceiniker S.E., Li P.W., Hoskins R.A., Galle R.F.,

RA Adams M.D., Ceiniker S.E., Li P.W., Hoskins R.A., Galle R.F.,

RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,

RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,

RA George R.A., Lewis S.E., Richards I. P., Abburner M., Pfeiffer B.D.,

RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,

RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,

RA Wan K.H., Doyle C., Baxter B.G., Helt G., Nelson C.R., Miklos G.L.G.,

RA Wan K.H., Doyle C., Baxter B.G., Helt G., Nelson C.R., Miklos G.L.G.,

RA Abril J.F., Apbayani A., An H.-J., Andrews-pfannkoch C., Baldwin D.,

RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,

RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,

RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier A., Chandra I.,

RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier A., Chandra I.,

RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,

RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier S.M.,

RA Bodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

RA Dodson K.J., Evangelista C.C., Perraz C., Perriera S., Pleischmann W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Sim
Matches 119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9V3Z1;
01-MAY-2000
01-MAY-2000
01-MAR-2003
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EUR. J. Biochem. 248:660-669(1997).
EMBL; AJ000480; CAA04119.1; -.
InterPro; IRR000719; Prot kinase.
Pfam; PP00069; pkinase; 1.
PROSUTE; PS50011; PROTEIN_KINASE_DOM; 1.
ATP-binding, Transferanc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=98000262; PubMed=9342215; Wilkin F., Suarez-Huerta N., Robaye Dumont J.B., Maenhaut C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATP-binding; Transferase.
NON TER 1 1
SEQUENCE 224 AA; 25479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ephydroidea; Drosophilidae;
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TRBL OR CG5408
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(TrEMBLrel. 13, Last sequence up
(TrEMBLrel. 23, Last annotation
BL protein (CG5408 protein).
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56.7%; Pred. No. 1.56
:ive 31; Mismatches
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RESULT Q8BFS7 ID Q8 AC Q8 DT 01 DT 01 DT 01

Q8BFS7; Q8BFS7; 01-MAR-2003 01-MAR-2003 01-MAR-2003

(TrEMBLrel. (TrEMBLrel. (TrEMBLrel.

Created)
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RA Glodek A., Gong P., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush P., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.B., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA McIkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA McIkulov G., Milshina N.V., Mobarry C., Morris J., Welson D.L.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier B., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,
RA Syirekas R., Tector C., Turner R., Venter B., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Milliams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-P., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.,
The genome sequence of Drosophila melanogaster.*;
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Best Local S
Matches 116
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Submitted (NOV-1999) to the EMBL/Ge
EMBL; AE003591; AAF51590.1; -
EMBL; AF204688; AAF26374.1; -
EMBL; AF204688; AAF26374.1; -
F1y9ase; FBgn0028978; trbl.
InterPro; IPR000719; Prot kinase.
Pfam; PF00069; pkinase; 1.
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PROSITE; PS50011; PROTEIN KINASE DOM; 1.

Hypothetical protein; ATP-binding; Transferase.

SEQUENCE 484 AA; 54077 MW; 3E3BLD3E5645B0D7
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                          LTATGILLHPWLRQDPMPLAPTRSHLWEAAQVVPDGLGLDEAREBEG
                                                                                                                                                        VWSLGVALFTMLAGHYPFQDSBFVLLFGKIRRGAYALPAGLSAPARCLVRCLLRRBPABR
                                                                                                                       MWSLGVILYTMLVGQYPFYBKANCNLITVIRHGNVQIPLTLSKSVRWLLLSLLRKDYTER
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Pred. No. 2.5e-28;
5; Mismatches 134;
-WSDABBDEG
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QBBJF ID QBBJF AC QBBJF AC QBBJF AC QBBJF DT 01-MB DT 01-MB GT SIMIJ DE (Freg QG Muse m CBI_RP SEQUE RC STRAIR A The ET RA THE LT RA THE LT RA ENBILL RA THE FRA THE F
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Q8BJR9;
01-MAR-2003
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STRAIN=C57BL/6J; TISSUE=Aorta and
MEDLINE=22354683; PubMed=12466851;
The PANTOM Consortium,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9BJR9;
01-MAR-2003 (TrEMBLrel. 23, Created;
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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Nature 420:563-573(2002).
RMBL; AK040738; BAC30668.1; -
EMBL; AK0407218; BAC30668.1; -
SEQUENCE 218 AA; 23907 MW; F3A5AFE
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STRAIN-675BL/6J; TISSUE-Aorta and MEDILINE-2234683; PubMed-12466851; The FANTOM CONBORTIUM,
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                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                  the RIKEN Genome Exploration Research "Analysis of the mouse transcriptome to,770 full-length cDNAs ";
Nature 420.563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                                                                               Pred. No. 2.8e-19;
3; Mismatches 79;
                                                                                                                                                                Score 326;
Pred. No. :
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Pred. No. 1.4e-19;
3; Mismatches 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus.
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Sciurognathi; Muridae;
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Mammalia; Eutheria; F
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STRAIN=C57BL/6J; TISSUE=Lung;
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Nature 420:563-573(2002).
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Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17.2%; Score 326; DB 11; 40.0%; Pred. No. 2.8e-19; Live 23; Mismatches 79
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GenCore version 5.1.6

Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on:

US-09-909-474D-2

Perfect score: 1891

Sequence: 1 MRATPLAAPAGSLSRKKRLE............GLGLDEAREEEGDREVVLYG 358

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 0

Maximum Match 100%

Listing first 45 summaries

Database: SwissProt_41:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Regult No.	Score	Query	Length	₽B	ID	Description
1	1887	99.8	358	<u>- </u>	NIPK HUMAN	Q96ru7 homo sapien
N	1345	71.1	354	_	NIPK_MOUSE	mune m
w	1331.5	70.4	349	_	NIPK_RAT	
۵	309	16.3	619	-	SNP1_CANTR	
Ç,	304.5	16.1	646	-	321	
o	304	16.1	620	_	SNFI_CANAL	
7	298.5	15.8	631	,_	CNK MOUSE	Q60806 mus musculu
8	291	15.4	615	_	CNK_RAT	
9	287	15.2	1518	μ	KKKI YEAST	_
10	284.5	15.0	611	_	SNP1 CANGA	Q00372 candida gla
11	281	14.9	512	_	KI 10 ARATH	
12	274.5	14.5	633	_	SNP1_YEAST	
13		14.5	533	_	KCCD_RAT	
14	271.5	14.4	593	_	CDR1_SCHPO	P07334 schizosacch
15	271	14.3	576	۳	SNF1_SCHPO	
16	269	14.2	542	-	KCCB_MOUSE	P28652 mus musculu
17	268	14.2	622	۲	YNA3_CABEL	
18	266.5	14.1	499	,	KCCD_HUMAN	Q13557 homo sapien
19	266	14.1	542	μ.	KCCB_RAT	
20	266	14.1	664	μ	KCCB_HUMAN	Q13554 homo sapien
21	253	13.9	1142	-	GIN4_YEAST	Q12263 Baccharomyc
22	261.5	13.8	552	_	AAK2_HUMAN	P54646 homo sapien
23		13.8	891	<u>ب</u>	KIN1_SCHPO	_
24	•	13.8	552	,_	AAK2_RAT	Q09137 rattus norv
25	260.5	٠	786	μ	SN1L_HUMAN	
26	ហ	٠	502	μ	RKI1_SECCE	
27	S	٠	610	μ	CDP1_ARATH	Q06850 arabidopsis
28	٠	13.5	478	۳	KCCA_HUMAN	
29	•	•	478	بر	KCCA_RAT	
30	252.5	13.4	433	μ	STKB_HUMAN	
31	ຫ	13.2	735	44	K6A1_RAT	•
32	247.5	13.1	685	ب	SNK HUMAN	
u	247	13.1	332	ب	AAIP_WHEAT	Q02066 triticum ae

45	44	43	42	41	40	39	38	37	36	35	3. 4.
240	240.5	241	242	242	242.5	243.5	243.5	243.5	244.5	244.5	246.5
12.7	12.7	12.7	12.8	12.8	12.8	12.9	12.9	12.9	12.9	12.9	13.0
682	548	542	915	661	353	529	527	472	735	478	724
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SNK MOUSE	AAK1_RAT	CDP3_ORYSA	KCC4_YBAST	Y537_HUMAN	ASK2_ARATH	KCCG_MOUSB	KCCG_RAT	KCCG_HUMAN	K6A1_HUMAN	KCCA_MOUSE	K6A1_MOUSE
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RA Klausher R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Parmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Usdin T.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Rodriguez A.C., Grinwood J., Schmutz J. M., Warra M.A.,
"Generation and initial analysis of more than 15,000 full-length
ruman and mouse cDNA sequences.",
"Generation and initial analysis of more than 15,000 full-length
ruman and mouse cDNA sequences.",
"Generation and initial analysis of more than 15,000 full-length
ruman and mouse colnA sequences.",
"Generation and initial analysis of more than 15,000 full-length
ruman and mouse colnA sequences.",
"Generation and initial analysis of more than 15,000 full-length
ruman and mouse colnA sequences.",
"Generation and initial analysis of more than 15,000 full-length
ruman and mouse colnA sequences.",
"Generation and initial analysis of more than 15,000 full-length
ruman and
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Best Local &
Matches 357
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EMBL; AK026945; BAB15597.1; -.
EMBL; AL034548; CAB81634.1; -.
EMBL; BC019363; AAH19363.1; -.
EMBL; BC027484; AAH27484.1; -.
Genew; HGNC1.16228; C2007£97.
InterPro; IPR000719; Prot_kinase
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SEQUENCE
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
TISSUB=cervix, and Muscle;
MEDLINE=22388257; PubMed=12477932;
MEDLINE=22388257; PubMed=12477932;
Grandle F.A., Gra
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SMART; SM00220;
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SIMILARITY: Contains 1 protein kinase domain.
                               121
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                                                                                                                                                                                                                                                                                                                                                                Similarity
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PDD00001, Prot kinase, 1.
9M00220, S TKC, 1.
7 P850011, PROTEIN_KINASE_DOM,
ARPTEVLAGTQLLYAFFTRTHGDMHSLYRSRHRIPEPEAAVLFRQMATALAHCHQHGLVL
                                                                                           MRATPLAAPAGSLSRKKRLELDDNLDTERPVQKRARSGPQPRLPPCLLPLSPPTAPDRAT
                                                                                                                                                                                                            MRATPLAAPAGSLSRKKRLELDDNLDTERPVQKRARSGPQPRLPPCLLPLSPPTAPDRAT
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1; Mismatches
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RA Okazaki Y., Furuno M., Kasito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Vagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Schriml E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Gantmond S., Gustincich S., Hirokawa Y., Kedzierski R.M., King B.L.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Magashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Magashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Magashima T., Reed J.C., Reed D.J., Reid J., Rang B.Z., Kingwald M.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Welle C.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Hara A., Hashizume W., Imotani K., Shihagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Mayashishi A., Waterston R., Lander B.S., Rogers J.,
RA Mara M., Shiraki Y.,
RA Mara M., Waterston R., Lander B.S., Rogers J.,
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Dower S.K.;

"Mammalian homologs of Drosophila tribbles

"Mammalian homologs of Drosophila tribbles

"Mammalian homologs of Drosophila tribbles

"Mammalian homologs of Drosophila tribbles
     MEDLINE=22388257; PubMed=12477932;
Strausberg R.L., Feingold E.A., Grouse L.H.,
Klausner R.D., Collins F.S., Wagner L., Shen
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                                                                                            sis of the mouse transcriptome full-length cDNAs."; 420:563-573(2002).
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Last annotation update)
nducible putative kinase
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L.A.J., Qwa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         databases.
                                                                                                                                     functional annotation
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       Schuler
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RA Distchenko L., Marusins K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Abramson R.D., Mullahy S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren R.J., Lu X., Gibbs R.A.,
RA Pahay J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Wyers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Wyers R.M.,
RA Schnerch A., Schein J.E., Jones S.J. M., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length
RT "Generation and initial analysis of more than 15,000 full-length
RT Thuman and mouse CDNA sequences."

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

1. PUNCTION: May play an important role in a common pathway leading
CC the programmed death of non-neuronal cells. May serve as an
endogenous antagonist competing for substrate with functional
CC kinases that act to promote neuronal cell survival (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local S
Matches 265
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CONFLICT
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial antities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Apoptosis.
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ProDom; PD000001; Prot_kinase; 1.
SMART; SM00220; S_TKC; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro, IPR000719; Prot kinase.
InterPro, IPR002290; Ser thr pkinase
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Hopkins R.F., Jordan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    similarity).
SIMILARITY: Contains 1 protein kinase domain.
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                                 RDLKLCRFVFADRERKKLVLENLEDSCVLTGFDDSLWDKHACPAYVGFEILSSRASYSGK
                                                                                                                                                                                                                           AVAPATRIGPYILLEREQGSCSYRALHCPTGTEYTCKYYPASEAQAVLAPYARLPTHQHV
                                                                                                                                                                                                                                                               AVATASRLGPYVLLEPEEGGRAYRALHCPTGTEYTCKVYPVQEALAVLEPYARLPPHKHV
                                                                                                                                                ARPTEVLAGTOLLYAFFTRTHGDMHSLVRSRHRIPEPEAAVLFROMATALAHCHOHGLVL
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RDLKLRRFVFSNCERTKLVLENLEDACVMTGSDDSLWDKHACPAYVGPEILSSRPSYSGK
                                                                                                               AR PTEVLLGSRLLY I PPTKTHGDLHSLVRSRRGI PESEAAGLFROMASA VAHCHKHGLVL
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ilarity 74.0%;
Conservative 2
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Pred. No. 3e-9
29; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROTEIN KINASE.

S -> P (IN REF. 3).

K -> T (IN REF. 1).

MISSING (IN REP. 3).

SERLVALGILLHEWLREDHGRVSPPQSDRREMDQVVPDGPQ
LEEAEEGEVGLYG -> CRATCGPGNPLASIVERGSRPSLS
STV (IN REF. 2).

2CB283PC119P859F CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                60;
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RESULT 3
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                                                                                                                                                                                                                                                                                    Query Match
Best Local S
Matches 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collable between the Swiss Institute of Bioinformatics and the EWBL outset the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for content is not removed.
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                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AB020967; BAA77582.1;
InterPro; IPR000719; Prot_k
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cell death.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-99262087; PubMed-10329375;
Mayumi-Matsuda K., Kojima S., Suzuki H., Sakata T.;
"Identification of a novel kinase-like gene induced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Neuronal cell death
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                                                                                                                                                                                                                                                                                                                                                                                                                                  PP00069; pkinase; 2.
pp00069; pkinase; 2.
pp. PD000001; Prot kinase; 1.
TTB: PS50011; PROTEIN KINASE DOM;
  116
                                                 121
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                                                                                                                                           61
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                                                                                                                                                                                                                                                                                                           Similarity
ARPTEVLLGSQLLYTFFTKTHGDLHSLVRSRRGIPEPEAAALPROMASAVAHCHKHGLIL
                        ARPTEVLAGTQLLYAFFTRTHGDMHSLVRSRHRIPBPBAAVLFRQMATALAHCHQHGLVL
                                                                                       AVAPATRIGPYILLEREQGICTYRALHCPTGTEYTCKYYPASEAQAVLAPYARLPTHQHV
                                                                                                                          AVATASRLGPYVLLEPEEGGRAYRALHCPTGTBYTCKVYPVQBALAVLBPYARLPPHKHV
                                                                                                                                                                                     MRATSLAASADVPCRKKPLEFDDNIDVECPVLKRVRDBPBPGPTPSL-----PPASDLSP
                                                                                                                                                                                                                             WRATPLAAPAGSLSRKKRLELDDNLDTERPVQKRARSGPQPRLPPCLLPLSPPTAPDRAT 60
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                                                                                                                                                                                                                                                                                                                                                                              63
349 AA;
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(Rel. 41,
(Rel. 41,
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Last annotation update)
nducible putative kinase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            _kinase.
                                                                                                                                                                                                                                                                                  26;
                                                                                                                                                                                                                                                                                                           Score 1331.5;
Pred. No. 3.4
                                                                                                                                                                                                                                                                                                                                                                                                         PROTEIN KINASE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
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SUPLY 4
SUPLY 6
SUPLY 
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    Query Match
Best Local &
Matches 95
                                                                                                                                                                                                                    InterPro; IPKUVALIA.

Pfam; PP00069; pkinase; 1.

ProDom; pD000001; Prot kinase; 1.

SMART; SM00220; S TKC; 1.

SMART; SM00220; S TKC; 1.

SMOSITE; PS00107; PROTEIN KINASE ATP; 1.

PROSITE; PS001108; PROTEIN KINASE T; 1.

PROSITE; PS00110; PROTEIN_KINASE T; 1.

PROSITE; PS50011; PROTEIN_KINASE DOM; 1.

PROSITE; PS50011; PROTEIN_KINASE DOM; 1.

Transferase; Serine/threonine-protein kinase; ATP-binding; Transferase; Serine/threonine-protein kinase; ATP-binding; Transferase; Carbohydrate metabolism; Nuclear protein.
                                                                                           DOMAIN
NP BIND
BINDING
ACT SITE
MOD RES
SEQUENCE
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15-JUL-1999
15-JUL-1999
15-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.

KANAI T., Ogawa K., Ueda M., Tanaka A.;

"Genetic evaluation of the function of SNF1 in Candida tropicali
"Genetic evaluation of the EMBL/GenBank/DDBJ databases.

1- PUNCTION: ESSENTIAL FOR RELEASE FROM GLUCOSE REPRESSION: IT
INTERACTS AND HAS FUNCTIONAL RELATIONSHLP TO THE REGULATORY
PROTEIN SNF4. COULD PHOSPHORYLATES CATE (BY SIMILARITY).

1- SUBCELLULAR LOCATION: ASSOCIATED WITH THE NUCLEAR MEMBRANE (
SIMILARITY): BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         use by non-profit institutions as long modified and this statement is not removed entitles requires a license agreement (See or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Saccharomycetales;
NCBI_TaxID=5482;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota; Pungi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Candida tropicalis (Yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Carbon catabolite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AB024535; BAA75889.1; -. HSSP; Q63450; 1A06.
                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR000719; Prot_kinase.
InterPro; IPR002290; Ser_thr_pkin
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                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBFAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AADVWSLGVALFTMLAGHYPFQDSEPVLLFGKIRRGAYALPAGLSAPARCLVRCLLRREP 300
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17
52
58
81
174
207
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(Rel.
    Conservative
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38, Last sequence update)
38, Last annotation updat
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66
81
174
207
                          16.3%;
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    48;
                                                                                         PROTEIN KINASE.

ATP (BY SIMILARITY).

ATP (BY SIMILARITY).

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

(BY SIMILARITY.

BY SIMILARITY.

BY GPCP1PC3DCE706D7 CRC64;
Score 309; DB
Pred. No. 8.5e-
48; Mismatches
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Saccharomycetales;
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                          DB 1;
.5e-17;
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    128,
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; Candida.
                                           Length
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    Indels
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    36;
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QPRLPPCLLPLSPPTAPDRATAVATASRLGPYVLLEP-BEG--GRAYRALHCPTGTEYTC

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HUMAN
                                                                                                   MEDLINE=98019242; PubMed=9353331;
Ouyang B., Pan H., Lu L., Li J., Star
Ouyang Br, Pan H., Lu L., Li J., Star
"Human Prk is a conserved protein ser
regulating M phase functions.";
J. Biol. Chem. 272:28646-28651(1997)
                                 MEDLINE=20027391; PubMed=1
Ouyang B., Li W., Pan H.,
"The physical association
phosphatase by Prk.";
                                                                                                                                                                                                        Lu L., D
 Oncogene 18:6029-6036(1999).
-I- FUNCTION: SERINE/THREONINE
PHASE FUNCTIONS DURING THE
                                                                              CHARACTERIZATION.
                                                                                                                                                             CHARACTER I ZATION.
                                                                                                                                                                                  "Prk, a cytokine-inducible human protein expression appears to be down-regulated i J. Biol. Chem. 271:19402-19408(1996).
                                                                                                                                                                                                                                         SEQUENCE OF 28-646 FROM TISSUE-Placenta; MEDLINE-96325053; PubMec
                                                                                                                                                                                                                                                                                       human macrophages.";
Oncogene 19:4832-4839(2000).
                                                                                                                                                                                                                                                                                                                                Holtrich U., Wolf G., Yun
Kauselmann G., Rehli M.,
                                                                                                                                                                                                                                                                                                                                                          MEDLINE=20493044;
                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota, Metazoa,
Mammalia, Butheria,
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                                            PubMed=10557092;
Pan H., Meadows J., Hoffmann
ociation and phosphorylation o
                                                                                                                                                                                                                           PubMed=8702627;
Pan H., Reissmann P.T.,
                                                                                                                                                                                                                                                                                                       expression
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Primates;
                                                                                                                                                                                                                                                                                                                                              Yuan
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Andreesen R., Kaufmann
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  PROTBIN KIN
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                                                                                                                           Stambrook P., Li |
| serine/threonine
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 CLB. MAY
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in lung carcinoman
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Y ALSO BE
                                             of Cdc25C
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M., Kuhl
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e kinase
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                                            W.,
C protein
 IN REGULATING PART OF THE
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Query Match
Best Local S
Matches 101
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GO; GO:0004674; P:protein as
GO; GO:0000468; P:protein an
GO; GO:0000074; P:regulation
InterPro; IRR000959; POLO bo
InterPro; IRR000719; Prote bo
InterPro; IRR000719; Prot bo
InterPro; IRR000719; Prot bo
InterPro; IRR000719; Prot bo
InterPro; IRR000719; Prot bo
InterPro; IRR000719; Polo box; 2...
Pronom: pro00659; POLO box; 2...
Pronom: pro00659; POLO box; 2...
                                                                                                                                                                                                                                                                                                                               Phosphorylation.
DOMAIN 62
NP BIND 68
BINDING 91
BINDING 91
BOMAIN 470
DOMAIN 567
CONPLICT 99
CONPLICT 419
CONPLICT 419
CONPLICT 464
                                                                                                                                                                                                                                                                                    NP BIND
BINDING
ACT SITE
DOMAIN
DOMAIN
CONFLICT
CONFLICT
CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Prodom; PD000001; Prot kinase; 1.

SMART; SM00220; S TKC; 1.

PROSITE; PS00107; PTCD BOX; 2.

PROSITE; PS00107; PROTEIN KINASE ATP; PROSITE; PS00101; PROTEIN KINASE DOM; PROSITE; PS00108; PROTEIN KINASE ST; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AJ293866; CAC10659.1; --
EMBL; U56998; AAC50637.1; ALT_INIT.
Genew; HGNC:2154; CNK.
GK; Q9H4B4; --
GK; Q9H4B4; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIGNALING NETWORK CONTROLLING CELLULAR ADHESION. IN VITRO, IS AB
TO PHOSPHORYLATE CDC25C AND CASEIN.

CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
SUBUNIT: BINDS TO THE CALCIUM/INTEGRIN-BINDING PROTEIN (CIB). TH
INTERACTION PROBABLY OCCURS VIA THE POLD-BOX DOMAIN.

SUBCELLULAR LOCATION: Membranc-associated.

TISSUE SPECIFICITY: TRANSCRIPTS ARE HIGHLY DETECTED IN PLACENTA,
LUNG, POLLOWED BY SKELETAL MUSCLE, HEART, PANCREAS, OVARIES AND
KIDNEY AND WEAKLY DETECTED IN LIVER AND BRAIN MAY HAVE A SHORT
HALF-LIVE. IN CELLS OF HEMATOPOIETIC ORIGIN, STRONGLY AND
EXCLUSIVELY DETECTED IN TERMINALLY DIFFERENTIATED MACROPHAGES.
TRANSCRIPTS EXPRESSION APPEARS TO BE DOWN-REGULATED IN PRIMARY
TRANSCRIPTS EXPRESSION APPEARS TO BE DOWN-REGULATED IN PRIMARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GO:0004674; P:protein serine/threonine kinase activity; TAS: GO:0006468; P:protein amino acid phosphorylation; TAS: GO:0000074; P:regulation of cell cycle; TAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INDUCTION: CYTOKINE AND CELLULAR ADHESION TRIGGER FNK INDUCTION PYM: PHOSPHORYLATED AS CELLS ENTER MITOSIS AND DEPHOSPHORYLATED CELLS EXIT MITOSIS (BY SIMILARITY).

SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES. CDC5/POLO SUBFAMILY.

SIMILARITY: Contains 2 POLO box domains.
    69
                                            69
                                                                                                                                              29
                                                                                                                                                                                                                   Similarity
                                                                                                                                         RPVQKRAR-----SGPQPRLPPCL------LPLSPP----TAPDRATAVATASRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TUMOR.
                                            GPYVLLEPEEGG--RAYRALHCPTGTEYTCKVYPVQEALAVLEPYARLP---
                                                                                              RPFORTAAATAPPAGPGP--PPSALRGPELEMLAGLPTSDPGRLITDPRSGRTYLKGRLL
                                                                                                                                                                                                                                                                               522
646
                                                                                                                                                                                          Conservative
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KGGFARCYEATDTETGSAYAVKVIPQSR----VVKPHQREKILNEIELHRDL
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76
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185
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                                                                                                                                                                                        48;
                                                                                                                                                                                                                                                                             PROTEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
POLO BOX 1.
POLO BOX 1.
POLO BOX 2.
V -> A (IN REF. 2).
V -> G (IN REF. 2).
V -> D (IN REF. 2).
H -> D (IN REF. 2).
FSEWUGF -> VSKWYDY (IN REF. PSEWUGF -> VSKWYDY (IN REF. 2).
R -> P (IN REP. 2).
                                                                                                                                                                                                                                                              S1...
LO BOX 1.
OLO BOX 2.
V -> A (IN REF. 2).
V -> G (IN REF. 2).
V -> D (IN REF. 2).
V -> D (IN REF. 2).
V -> C (IN REF. 2).
                                                                                                                                                                                                                 Score 304.5; DB 1;
Pred. No. 2e-16;
                                                                                                                                                                                          Mismatches
                                                                                                                                                                                        134;
                                                                                                                                                                                        Indels
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tions on its
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RESULT 6
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C STRAIN-ATCC 32354 / B-311;

A Petter R., Kwon-Chung K.J.;

L Submitted (MAR-1996) to the EMBL/GenBank/DDBJ databases.

C --- FUNCTION: ESSENTIAL FOR RELEASE FROM GLUCOSE REPRESSION. IT

INTERACTS AND HAS FUNCTIONAL RELATIONSHIP TO THE REGULATORY

PROTEIN SNP4. COULD PHOSPHORYLATES CATS (BY SIMILARITY).

SUBCELLULAR LOCATION: ASSOCIATED WITH THE NUCLEAR MEMBRANE (BY SIMILARITY).

BIMILARITY: BELONGS TO THE COURTS.
EMBL; L78129; AAB48643.1; ...
EMBL; L39263; AAA92456.1; -..
HSSP; Q63450; 1A06.
InterPro; IPR000719; Prot kinase.
InterPro; IPR0002290; Ser thr_pkinase.
Pfam; PF00069; pkinase; 1.
ProDom; PD000001; Prot kinase; 1.
PRODOM; PB000107; PROTEIN_KINASE_ST; 1.
PROSITE; P800107; PROTEIN_KINASE_ST; 1.
PROSITE; PS0011; PROTEIN_KINASE_TOM; 1.
PROSITE; PS0011; PROTEIN_KINASE_DM; 1.
PROSITE; PS0011; PROTEIN_KINASE_DM; 1.
PROSITE; PS0011; PROTEIN_KINASE_DM; 1.
                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outsit the EMBLogean Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (see http://www.isb-sib.ch/anor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-1996 (Rel. 34, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
30-MAY-2000 (Rel. 39, Last amotation updat
Carbon catabolite derepressing protein kina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRALIN-ATCC 32354 / B-311;
STRALIN-ATCC 32354 / B-311;
MEDLINE-98063924, PubMed=9393775;
Petter R., Chang Y.C., Kwon-Chung K.J.;
Petter R., Chang 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Saccharomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bukaryota; Fungi; Ascomycota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P52497;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CANAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SRASYSGKAADVWSLGVALFTMLAGHYPPQDSBPVLLFGKIRRGAYALPAGLSAPARCLV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QHRHIVRFSHHFEDADNIYIFLELCSRKSLAHIWKARHTLLEPBVRYYLRQILSGLKYLH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Saccharomycotina; Saccharomycetes; Saccharomycetales; Candida.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
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protein kinase
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                                  kinase;
     ATP-binding;
lear protein.
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EMBL outstation -
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RESULT 7
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Matches 95
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CONFLICT
SEQUENCE
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DOMAIN
NP BIND
BIND
BIND
BITE
ACT SITE
MOD RES
CONFLICT
CONFLICT
          Submitted [3]
                                                                        MEDLINE=95247749; PubMed=7730342; Donohue P.J., Albarts G.F., Guo Y., Winkles J.A.; Donohue P.J., Albarts G.F., Guo Y., Winkles J.A.; "Identification by targeted differential display of gene encoding a putative serine/threonine kinase." J. Biol. Chem. 270:10351-10357(1995).
                                                                                                                                                                                                                              O60806; Q60822; Q9R009;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-PEB-2003 (Rel. 41, Last annotation update)
Cytokine-inducible serine/threonine-protein k
                                                                                                                                                           Eukaryota, Metazoa, Chordata,
Mammalia, Eutheria, Rodentia,
MCBI_TaxID=10090,
                                                                                                                                                                                                          inducible kinase).
                               STRAIN=NIH
Kauselmann
                                                                                                                               SEQUENCE FROM N.A.
STRAIN=NIH Swiss;
                                                                                                                                                                                                                                                                                       CNK_MOUSE
FUNCTION,
                                                      BEQUENCE
                                                                                                                                                                                                Mus musculus (Mouse)
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                   OF 333-437 FROM N.A. (ISOFORM IH SW188; 
The Swider M., Kuhl D.; 
d (NOV-1999) to the EMBL/GenBar
                                                                                                                                                                                                                                                                                                                                           DYLLPPDLSKNKNSKIDVDBDVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                   LWDKHAC--PAYV-GPEILSSRASYSGKAADVWSLGVALPTWLAGHYPPQDSBPVLLFGK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LPLSPPTAPDRATAVATASRLGPYVLLEP-EEG--GRAYRALHCPTGTEYTCKVYPVQEA
                                                                                                                                                                                                                                                                                                                                                                                                                                   NFLKTSCGSPNYMPAPEVISGKL-YAGPEVDVWSAGVILYVMLCGRLPFDDEFIPALFKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EDEARRFFQQIIAAVEYCHRHKIVHRDLKPENLLLDDQLNVKIADFGL--SNIMT---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EPBAAVLFROMATALAHCHOHGLVLRDLKLCRFVFADRERKKLVLENLEDSCVLTGPDDS
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                                                                                                                                                                                                                                                                                                                                                                  AQVVPDGLGLDEAREEEGDREVV 355
                                                                                                                                                                                                                                                                                                                                                                                        ISNGVYTLPNYLSAGAKHLLTRMLVVNPLNRITIHBIMEDDWPKQD-MP-
                                                                                                                                                                                                                                                                                                                                                                                                    IRRGAYALPAGLSAPARCLVRCLLRREPAERLTATGILLHPWLRQDPMPLAPTRSHLWEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         <u>LAKSDMQGRVEREISYLRLLRHPHIIKLYDVIKSKDEIIMVIEFAGKELFDYIVQRGKMP</u>
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59
175
208
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PHOSPHORYLATION
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416
494
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67
82
175
208
234
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29.4%;
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PQ -> AR (IN REF. 2).
AGPBUDV -> SEVGKLMI (IN REF. 2).
YVMLCGRLPPDDEF -> GMSCCVVDYHSMTSS (:
REF. 2).
A -> A (IN REF. 2).
S -> L (IN REF. 2).
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                      EMBL/GenBank/DDBJ
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PROTEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 304; DB 1;
Pred. No. 2.1e-16;
5; Mismatches 131
                                                                                                                                                                         Craniata; Vertebrata;
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1806C652B5061D2B CRC64;
                                                                                                                                                                                                                                                                                        631
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                    databases
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                                                                                      of an
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                                                                                                                                                                         Euteleostomi; ; Murinae; Mus
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                                                                                                                                                                                                                                 2.7.1.37) (FGF-
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                                                                                                                               Query Match
Best Local S
Matches 98
                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000959; POLO_box.
InterPro; IPR000719; Prot_kinase.
InterPro; IPR000719; Prot_kinase.
InterPro; IPR002290; Ser_thr_pkinase.
InterPro; IPR002290; Ser_thr_pkinase.
Pfam; PP00059; Pkinase; 1.
Pfam; PP00059; POLO_box; 2.
ProDom; PP000001; Prot_kinase; 1.
SMART; SM00220; S TKG; 1.
SMART; SM00220; S TKG; 1.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00101; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00101; PROTEIN_KINASE_TOM; 1.
PROSITE; PS00101; PROTEIN_KINASE_ST; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
PROSITE
                                                                                                                                                                                                                                                                                      Phosphorylation; DOMAIN 63

DOMAIN 63

NP BIND 69

BINDING 92

BOTH 186

DOMAIN 455

DOMAIN 552

DOMAIN 553
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"Expression and phosphorylation of fibroblast-growth-factor-inducible kinase (Fnk) during cell-cycle progression.";
Blochem. J. 33:655-660(1998).

-1- FUNCTION: SERIME/THREONIE PROTEIN KINASE INVOLVED IN REGULATING IPPROTEIN GROWTH CELL CYCLE. MAY ALSO BE PART OF THE SIGNALING NETWORK CONTROLLING CELLULAR ADHBSION. IN VITRO, IS ABLITO PHOSPHORYLATE CDC25C AND CASEIN (BY SIMILARITY).

-1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
-1- SUBUNIT: BINDS TO THE CALCIUM/INTEGRIN-BINDING PROTEIN (CIB). THIS INTERACTION PROBABLY OCCURS VIA THE POLO-BOX DOMAIN (BY
                                                                                                                                                                                                                       CONFLICT
                                                                                                                                                                                                                                                                                    ACT SITE
DOMAIN
DOMAIN
VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a clear the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and foentities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIR; A57286; A57286.
MGD; MGI:109604; Cnk.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AF136586; AAF08369.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; U21392; AAC52191.1; -.
EMBL; U22434; AAC52192.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ÷
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ISOId=Q60806-2; Sequence=VSP_004927; TISSUB_SPECIFICITY: EXPRESSED_IN_SKIN.
PTM: PHOSPHORYLATED AS CELLS ENTER MIT
CELLS EXIT MITOSIS.
SIMILARITY: BELONGS TO THE SER/THR FAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBCELLULAR LOCATION: Membrane-associated ALTERNATIVE PRODUCTS: Event=Alternative splicing; Named isoforms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY: Contains 2 POLO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CDC5/POLO SUBFAMILY
                                              50
  78
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                                                                                                                                                         Similarity
                                         PRP-FPRAAVPSAPPAGPG---PPANASPRSEPEVLAGPRAPDPPGRLITDPLSGRTYTK
                                                                                     POPRLPPCLLPLSPPTAPDRATAVATAS-RLGPYVLLEPE-----
                                                                                                                             15.8%;
ilarity 28.3%;
Conservative 4
EGG--RAYRALHCPTGTEYTCKVYPVQBALAVLBPYARLP
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77
92
186
518
622
373
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                                                                                                                                  40;
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                                                                                                                                                                                                                 ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
POLO BOX 1.
POLO BOX 2.
L -> LVSGLARTSIGHPDVRPB (ir
/FTId=VSP 004927.
I -> V (IN RBF. 2).
W; 20857341870DB1D2 CRC64;
                                                                                                                                                    Score 298.5;
Pred. No. 5.0
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ATP (BY
                                                                                                                                  Mismatches
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                                                                                                                                                      8e-16;
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RESULT 8
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                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                  use by non-profit instituted modified and this statement entities requires a license or send an email to licensea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=99452760; PubMed=10523297;
Kauselmann G., Weller M., Wulff P., Jessberger S., Konietzko
Kauselmann G., Staubli U., Bereiter-Hahn J., Strebhardt K., Kuhl
"The polo-like protein kinases Fnk and Snk associate with a (
"The polo-like protein and are regulated dynamically with a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CNK_RAT STANDARD; PRT; 615 AA. (99R011; 16-OCT-2001 (Rel. 40, Created) 16-OCT-2001 (Rel. 40, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) Cytokine-inducible serine/threonine-protein kinase inducible kinase) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata;
Memmalia; Eutheria; Rodentia;
NCBI_TaxID=10116;
                 InterPro
                                    InterPro;
                                                  EMBL, AF136584; AAF08367.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         plasticity.",
EMBO J. 18:5528-5539(1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE PROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CNK OR PNK.
                                                                                                                                                                                                                                                                                                                                  FUNCTION: SERINE/THREONINE PROTEIN KINASE INVOLVED IN REGULATING PHASE FUNCTIONS DURING THE CELL CYCLE. MAY ALSO BE PART OF THE SIGNALING NETWORK CONTROLLING CELULLAR ADRESION. IN VITRO, IS ABLIO TO PHOSPHORYLATE CDC25C AND CASEIN (BY SIMILARITY).

CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein. SUBUNIT: BINDS TO THE CALCIUM/INTEGRIN-BINDING PROTEIN (CIB). THI INTERACTION PROBABLY OCCURS VIA THE POLO-BOX DOMAIN.

SUBCELLULAR LOCATION: WHEN INDUCED, IT TRANSLOCATES INTO THE DENNEITES OF ACTIVATED NEURONS.
                                                                                                                                                                                                                    INDUCTION: BY THE INTENSE ACTIVITY ASSOCIATED PTM: PHOSPHORYLATED AS CELLS ENTER MITOSIS AND CELLS EXITY MITOSIS (BY SIMILARITY). SIMILARITY: BELONGS TO THE SER/THR FAMILY OF FCDC5/POLO SUBFAMILY.
SIMILARITY: Contains 2 POLO box domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   297
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                                                                                  an email to license@isb-sib.ch).
   ; IPR000959; ; IPR000719; ; IPR002290;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LHRDLKLGNFFITD--NMBLKVGDFGLAARLBPPEQR--KKTICGTPNYVAPEVLLRQG-
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POLO_box.
Prot_kinase.
Ser_thr_pkinase
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Sciurognathi; Muridae;
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                                                                                                    (See http://www.isb-sib.
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/ Murinae; Rattus.
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RESULT 9
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Best Local Similarity
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NP BIND
BINDING
ACT SITE
DOMĀIN
DOMAIN
NON TER
SEQÜENCE
                                                   MEDLINE-94078677; PubMed-8256524;
Pallier C., Valene M., Puzoe V.,
Bolotin-Fukuhara M.;
                                                                                                                             Saccharomyces cerevisiae (Baker's yeast).
Bukaryota, Fungi, Ascomycota; Saccharomycotina, Saccl
Saccharomycetales; Saccharomycetaceae; Saccharomyces
                                                                                                                                                           01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequenc
30-MAY-2000 (Rel. 39, Last annotat
Probable serine/threonine-protein
YKL101W OR YKL453.
            kinases.";
                              "DNA sequence analysis of a 17 kb fragment of yeast chromosome XI physically localizes the MRB1 gene and reveals eight new open rea
                                                                                               SEQUENCE PROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Phospho
NON TER
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SMART; SM00220; S TKC; 1.
PROSITE; PS50078; POLO BOX; 2.
PROSITE; PS00107; PROTEIN KINASE ATP;
PROSITE; PS00101; PROTEIN KINASE ST; 1
PROSITE; PS00108; PROTEIN KINASE ST; 1
Transferase; Serine/threomine-protein
 Yeast
                                                                                                                                                                                                                   P34244;
                                                                                                                                                                                                                              KKK1 YEAST
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                                                                                                                  _TaxID=4932;
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9:1149-1155(1993)
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                   including
                                                                                                                                                                                                                                                                                    DFFTKGYTPDRLPVS-----
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37
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154
440
537
615
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(Rel. 28, Last sequence up
(Rel. 39, Last annotation
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                    a homologue
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; Pred. No. 2.2e-15;
47; Mismatches 127
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ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
POLO BOX 1.
POLO BOX 2.
                    gene and reveals of the KIN1/KIN2
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                                                             Pukuhara H.,
                                                                                                                                                                        cion update)
kinase YKL101W
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                    and
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                                                                                                                                        Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length
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                    SNP1
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                              reading
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RESULT 10
SNF1_CANGA
ID SNF1_CANGA
AC Q00372;
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Best Local &
Matches 86
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R EMBL; Z28101; CAA81941.1; -.

R PIR; S37928; S37928.

R HSSP; Q63450; 1A06.

R SGD; 90001584; HSL1.

GG; GG:0005940; C:septin ring; IDA.

GG; GG:0005940; C:septin ring; IDA.

GG; GG:0000594; P:g2/M transition of mitotic cell cycle; IGI.

R GG; GG:0000074; P:regulation of cell cycle; IGI.

R GG; GG:0000074; P:regulation of cell cycle; IMP.

R GG; GG:0000074; P:regulation of cell cycle; IMP.

R GG; GG:0000135; P:septin checkpoint; IGI.

R InterPro; IPR000719; Prot kinase.

R InterPro; IPR001245; Tyr_pkinase.

R InterPro; IPR001245; Tyr_pkinase.

R Pfam; PF00069; pkinase; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PRO0109; TYRKINASE.

ProDom; PD000001; Prot_kinase; 1.

SMART; SM00220; S_TKC; 1.

PROSITE; PS00107; PROTEIN KINASE_ST; 1.

PROSITE; PS00109; PROTEIN_KINASE_ST; 1.

PROSITE; PS00101; PROTEIN_KINASE_DOM; 1.

Hypothetical protein; Transferase; Serine/threonine-protein ATP-binding.
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NP BIND
BINDING
ACT SITE
SEQUENCE
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                                                                                                          ERLTATGILLHPWLRQ-DPMPL:|:|:| | | | | | ::: | :|: | :|: | | :|: | | :|: | | :|: | | :|: | | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: |
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                                                                                                                                                                                                        ADVWSLGVALFTMLAGHYPFQDSEPVLLFGKIRRGAYALFAGLSAFARCLVRCLLRREFA
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                   STANDARD;
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ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
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Pred.
                   PRT;
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                                                                                                                                              322
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ed. No. 1.3e-14;
Mismatches 128
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803F84F7531241DD CRC64;
                   611
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               199
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Query Match
Best Local S
Matches 90
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01-NOV-1997
15-JUL-1999
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DOMAIN
NP BIND
BINDING
ACT SITE
MOD RES
SEQUENCE
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Candida
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Probom; PD000001; Prot_kinase; 1.

SMART; SM00220; S_TKC; I.

PROSITE; PS00107; PROTEIN_KINASE_ATP,

PROSITE; PS00108; PROTEIN_KINASE_DOM;

PROSITE; PS50011; PROTEIN_KINASE_DOM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pathogenic yeast Candida
Infect. Immun. 64:5269-52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota; Pungi; 1
Saccharomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; L78130; AAB48642.1; -.
HSSP; P24941; 1HCL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Petter R., Kwon-Chung K.J.;
"Disruption of the SNF1 gene abolishes trehalose utilization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=97101049; PubMed=8945576;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N
STRAIN-NCCLS84;
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InterPro; IPR002290; Ser_thr_pkir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             inogenic yeast Candida glabrata.";

eet. Immun. 64:5269-5273 (1996).

FUNCTION: ESSENTIAL FOR RELEASE FROM GLUCOSE REPRESSION. IT
INTERACTS AND HAS FUNCTIONAL RELATIONSHIP TO THE REGULATIONY
PROTEIN SUP4. COULD PHOSPHORYLATES CATS (BY SIMILARITY).

SUBCELLULAR LOCATION: ASSOCIATED WITH THE NUCLEAR MEMBRANE (SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES
144
                                     165
                                                                                                             110
                                                                          84
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                                                                                                                                                  25
                                                                                                                                                                                                                           90;
                                                                                                                                                                                                                                          Similarity
QIISAVEYCHRHKIVHRDLKPENLLLDEHLNVKIADFGL--SNIMT
                   QMATALAHCHQHGLVLRDLKLCRFVFADRERKKLVLENLEDSCVLTGPDDSLWDKHAC---
                                                                        IDREISYLRLLRHPHIIKLYDVIKSKDEIIMVIEYAGNELFDYIVQRNKMSEQBARRFFQ
                                                                                                           ----PYARLPPHKHVARPTEVLAGTQLLYAFFTRTHGDMHSLVRSRHRIPBPBAAVLFR
                                                                                                                                                NKVSSLADGSRVGNYQIVKTLGEGSFGKVKLAYHVTTGQKVALKSIN-KKVLAKSDMQGR
                                                                                                                                                                                   DRATAVATASRLGPYVLLEP-EEG--GRAYRALHCPTGTEYTCKVYPVQEALAVLE----
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45
68
161
194
611
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(Rel.
(Rel.
                                                                                                                                                                                                                           Conservative
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0011; PROTEIN KINASE DOM; 1.
Serine/threomine-protein kinase;
ion; Carbohydrate metabolism; Nucl
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; Ascomycota; Saccharomycotina; ;
s; mitosporic Saccharomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           . 35, Created)
. 35, Last sequ
. 38, Last annot
e derepressing |
                                                                                                                                                                                                                                                                                                                     17
290
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194
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27.9%;
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Last annotation update)
epressing protein kinase
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                                                                                                                                                                                                                         54;
                                                                                                                                                                                                                         Score 284.5; | Pred. No. 7e-1:
                                                                                                                                                                                                                                                                                                                 PROTEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                               POLY-HIS
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                                                                                                                                                                                                                                                          DB 1;
                                                                                                                                                                                                                         136;
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lear protein.
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                                                                                                                                                                                                                                                                                                   CRC64;
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DGNFLKTSCGS
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198
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                                 222
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RESULT 11

KI10 ARATI
ID XI10

AC 03830

AC 04830

AC 04
                                                                                                                                                                                                                              RX MEDLINES=21016720) FubMed=11130713;
RX MEDLINES=21016720) FubMed=11130713;
RA Fartmann B., Valle G., Bloecker H., Perez-Alonso M., Obermaier B.,
RA Fartmann B., Valle G., Bloecker H., Perez-Alonso M., Obermaier B.,
RA Delseny M., Boutry M., Grivell L.A., Mache R., Puigdomenech P.,
RA Delseny M., Boutry M., Grivell L.A., Mache R., Puigdomenech P.,
RA Wincker P., Cattolico L., Weissenbach J., Saurin W., Quetter P.,
RA Wincker P., Cattolico L., Weissenbach J., Saurin W., Quetter P.,
RA Wincker P., Cattolico L., Weissenbach J., Saurin W., Quetter P.,
RA Wincker P., Cattolico L., Weissenbach J., Saurin W., Quetter P.,
RA Wincker P., Cattolico L., Weissenbach J., Saurin W., Quetter P.,
RA Wincker P., Cattolico L., Weissenbach J., Brandt P., Nyakatura G.,
RA Wincker P., Cangelo M., Pallavicini A., Toppo S., Simionati B.,
RA Wincker P., Cangelo M., Pallavicini A., Toppo S., Simionati B.,
RA Conrad A., Hornischer K., Kauer G., Loehnert T.-H., Nordsiek G.,
RA Reichelt J., Scharfe M., Schoen O., Bargues M., Terol J., Climent J.,
RA Rooney T., Collado C., Perez-Perez A., Ottenwaelder B., Duchemin D.,
RA Mannhaupt G., Haase D., Schoof H., Rudd S., Zaccaria P., Mewes H.-W.,
RA Mannhaupt G., Haase D., Schoof H., Rudd S., Zaccaria P., Mewes H.-W.,
RA Mayer K.P.X., Kaul S., Town C.D., Koo H.L., Tallon L.J., Jenkins J.,
RA Rooney T., Haase B., Maiti R., Wu D., Peterson J., Van Aken S.,
RA Prauser C.M., Kaneko T., Nakamura Y., Sato S., Kato T., Asamizu B.,
RA Fraser C.M., Kaneko T., Nakasania K., Kawashima K., Kishida Y.,
RA Sasamoto S., Kimura T., Idesawa K., Kawashima K., Kishida Y.,
RA Watanabe A., Yamada M., Yasuda M., Tabata S.;
RT "Sequence and analysis of chromosome 3 of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              용
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Q3897; 004728, Q39076;
15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-SBP-2003 (Rel. 42, Last sunctation update)
15-SBP-2003 (Rel. 42, Last sunctation update)
SNF1-related protein kinase KIN10 (EC 2.7.1.-) (AKIN10).
KIN10 OR SKIN10 OR A73G01090 OR 74P13.22.
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II, Brassicales; Brassicaceae; Arabidopsis.
MEDLINE=95115691; PubMed=7816049; le Guen L., Thomas M., Kreis M.;
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MEDLLNB=93013041, PubMed=1339373;

MEDLLNB=93013041, PubMed=1339373;

1e Guen L., Thomas M., Bianchi M., Halford N.G., Kreis M.;

1e Guen L., Thomas M., Bianchi M., Halford N.G., Kreis M.;

"Structure and expression of a gene from Arabidopsis thaliana encoding a protein related to SNF1 protein kinase.";

Gene 120:249-254(1992).
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Submitted (DEC-1996) (
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Matches
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EMBL; X79707; CAA56146.1; -.
EMBL; AC008261; AAF26155.1; -.
EMBL; X94757; CAA64384.1; -.
PIR; JC1446; JC1446.
HSSP; Q63450; 1A06.
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DOMAIN 19
DOMAIN 299
NP BIND 25
BINDING 48
ACT SITS 145
MOD_RES 175
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BINDING
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Pfam; PP00627; UBA; 1.
PRINTS; PR00109; TYRKINASE.
ProDom; PD000001; Prot_kinase;
SMART; SM00220; S TKC; 1.
SMART; SM00165; UBA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the EMropean Bioinformatics Institute. There are no restrues by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entitles requires a license agreement (See http://www.isb-sor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS001107; PROTEIN KINASE ATP; PROSITE; PS50011; PROTEIN KINASE DOM; PROSITE; PS001108; PROTEIN KINASE_ST; PROSITE; PS50030; UBA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR001772; Kinase Cterm.
InterPro; IPR002719; Prot kinase.
InterPro; IPR002790; Ser_thr_pkinase.
InterPro; IPR001245; Tyr_pkinase.
InterPro; IPR000449; UBA_domain.
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thaliana genome.";
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TISSUE SPECIFICITY:
SIMILARITY: BELONGS
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AGTQLLYAFFTRTH-GDMHSLVRSRHRIPEPEAAVLFRQMATALAHCHQHGLVLRDLK--
                                                                                                                                                        NLLLDSKCNVKIADFGLSNIMRDGHFLKTSC
                                                               YAGPEVDVWSCGVILYALLCGTLPFDDENIPNLFKKIKGGIYTLPSHLSPGARDLIPRML
                                                                                                        YSGKAADVWSLGVALFTMLAGHYPFQDSEPVLLFGKIRRGAYALPAGLSAPARCLVRCLL
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BY SIMILARITY.
PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
5A18655A0AA506DP CRC64;
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RESULT 12
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01-JAN-1988 (Rel. 06, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
Carbon catabolite derepressing protein kinase (EC 2.7.1.-).
SNP1 OR CAT1 OR CCR1 OR PAS14 OR GLC2 OR YDR477W OR D8035.20.
Saccharomyces cerevisiae (Baker's yeast).
Bukaryota, Pungi, Ascomycota, Saccharomycotina, Saccharomycetes,
Saccharomycetteles, Saccharomycetaceae, Saccharomycees.
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EMBL; M13971; AAA35058.1; -.
EMBL; U33050; AAB66304.1; -.
EMBL; U33050; AAB6630.
HSSP; P24941; 1HCL.
SGD; S0002885; SNP1.
GO; GO:0005634; C:vtcleus; IPI.
GO; GO:0005634; C:vacuole (sensu Fungi); IPI.
GO; GO:0004679; F:NPIA/AMP-activated protein kinase activity;
GO; GO:0006468; P:protein amino acid phosphorylation; IDA.
GO; GO:0006955; P:cesponse to nitrogen starvation; IDA.
InterPro; IPR000719; Prot_kinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           District F.S., Mulligan J., Allen E., Araujo R., Aviles E., Berno A., Carpenter J., Chen E., Cherry J.M., Chung B., Dunce Hunicke-Smith S., Hyman R., Komp C., Lashkari D., Lew H., Lit Mosedale D., Nakahara K., Namath A., Oefner P., Oh C., Petal Roberte D., Schramm S., Schroeder M., Shogren T., Shroff N., Winant A., Yelton M., Botstein D., Davis R.W.; Submitted (AUG-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "A yeast gene that is essential encodes a protein kinase."; Science 233:1175-1180(1986).
                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/anor send an email to license@isb-sib.ch).
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Katels P., Witters L.A., Kemp B.B.;
"Mammalian AMP-activated protein kin
functional homology with the catalyt
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MEDLINE=86289463; Publ
Celenza J.L., Carlson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SNP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BIOL Chem. 269:2361-2364(1994).

FUNCTION: ESSENTIAL FOR RELEASE FROM GLUCOSE INTERACTS AND HAS FUNCTIONAL RELATIONSHIP TO PROTEIN SNF4. INTERACTS ALSO WITH SIP1, SIP2 PHOSPHORYLATES CAT8.
SUBCELLULAR LOCATION: ASSOCIATED WITH THE NUC SIMILARITY: BELONGS TO THE SER/THR FAMILY OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YEAST
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OF PROTEIN KINASES
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O THE REGULATORY
2 AND GAL83. COUL
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Best Local S
Matches 88
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P15791;
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01-APR-1990
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SMART; S
SEQUENCE OF 314-533 FROM N.A.
SEQUENCE OF 314-533 FROM N.A.
STRAIN-Sprague-Dawley; TISSUE-Aorta, and S
MEDLINE-93300844; PubMed-8390994;
MEDLINE-93300844; PubMed-8390994;
MEDLINE-Sprague-Dawley; Tissue-Aorta, and S
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PROSITE; PS00108; PROTEIN KINASE ST; 1.
PROSITE; PS50011; PROTEIN KINASE DM; 1.
Transferase; Serine/threonine-protein kin
Phosphorylation; Carbohydrate metabolism;
DOMAIN
18
32
POLY-HIS.
                                                                                                                                                                                                                                                                      Rattus norvegicus (Rat).
Bukaryota; Metazoa; Chordata;
Mammalia; Butheria; Rodentia;
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28-PBB-2003 (Rel. 41, Last annotation update)
Calcium/calmodulin-dependent protein kinase t
(EC 2.7.1.123) (CaM-kinase II delta chain) (C
                                                                                                                             protein
                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE=90036861; PubMe
Tobimatsu T., Fujisawa
"Tissue-specific expres
                                                                                                                                                                                                                                                                                                                                                          subunit) (CaMK-II delta subunit).
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Pfam; PF00069; pkinas
                                                                                                                                                                                                                                                  NCBI_TaxID=10116;
                                                                                                            Biol.
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                                                                                                        -specific expression of four kinase II mRNAs."; Chem. 264:17907-17912(1989)
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(Rel. 14, Last sequence up
(Rel. 41, Last annotation)
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ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
PHOSPHORYLATION (AUTO-).
PHOSPHORYLATION (AUTO-).
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Pred. No. 4.4e-14;
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Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
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lear protein.
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Query Match
Best Local S
Matches 79
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J. Biol. Chem. 268:14443-14449(1993).

-I. FUNCTION: THIS KINASE MAY PLAY A ROLE IN NEUROTRANSMISSION.
-I. CATALYTIC ACTIVITY: ATP + protein = ADP + O-phosphoprotein.
-I. ENZYME REGULATION: AUTOPHOSPHORYLATION OF CAM-KINASE II PLI-
IMPORTANT ROLE IN THE REGULATION OF THE KINASE ACTIVITY.
-I. SUBUNIT: COMPOSED OF FOUR DIFFERENT CHAINS: ALPHA, BETA, G
                                                                                                                                                                                                                                                                                                                                BINDING
ACT SITE
DOMĀIN
                                                                                                                                                                                                                                                                                                                                                                                                                 ProDom; PD000001; Prot kinase; 1.

SMART; SM00220; S TKC; 1.

PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

PROSITE; PS00108; PROTEIN_KINASE_ST; 1.

PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.

Transferase; Serine/threonine-protein kinase; Calmodulin-binding; Phosphorylation; ATP-binding; Neurone; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    entities
or send a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entre the European Bioinformatics Institute. There are no restrate by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
                                                                                                                               SEQUENCE
                                                                                                                                                                   VARSPLIC
                                                                                                                                                                                                        VARSPLIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Identification of novel isoforms Ca2+/calmodulin-dependent protein
                                                                                                                                                                                                                                                                                                                VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro, IPR000719; Prot_kinase.
InterPro, IPR002290; Ser thr_pkinase.
Pfam; PP00069; pkinase; I.
ProDom; PD000001; Prot_kinase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIR, A34366, A34366.
HSSP; Q63450, 1A06.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MUSCLE.
SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
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                      61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IsoId=P15791-1; Sequence=Displayed;
                                                         1 Similarity 79; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BOId=P15791-3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BOId=P15791-2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g requires a license agreement (See http://www.isb-sib.ch/announce/
an email to license@isb-sib.ch).
AVATASRLGPYVLLEPEEGGRAY----RALHCPTGTBYTCKVYPVQEALA----VLEPYA 112 : | : | : | : | : | | | |
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ilarity 28.8%;
Conservative 5
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                                                         53;
                                                                                                                                                                                                                                                     ATP (BY SIMILARITY).

BY SIMILARITY.
CALMODULIN-BINDING (BY SIMILARITY).
Missing (in isoform Delta 2).
/FTId=VSP_004784.
INNKANV -> KRKSSSV (in isoform Delta /FTId=VSP_004785.
                                                                                                                         Missing (In isoform Delta 3).
/PTId=VSP_004786.
GNK -> QMM (in isoform Delta 3
/PTId=VSP_004787.
Missing (In isoform Delta 4).
/PTId=VSP_004788.
W, B41BCB2B5A00B7CA CRC64;
                                                       Score 273.5; | Pred. No. 4.3e | 53; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                          PROTEIN KINASE
                                                                                                                                                                                                                                                                                                                                                                      (BY SIMILARITY).
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No. 4.3e-14;
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                                                         Indels
                                                                                       Length
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RA Wood V. Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gollins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA James K., Jones M., Leather S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Oliver K., O'Neil S., Pearson D., Quail M.A., Rabbinowitsch B.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Moodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA Weltjens I., Vanstreels B., Rieger M., Schaefer M., Meller-Auer S.,
RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA Weltjens I., Vanstreels B., Rieger M., Schaefer M., Meller-Auer S.,
RA Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
RA Geffeau A., Cadieu B., Dreano S., Gloux S., Lehrach B.M.,
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
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SCHPO
STANDARD;

CDR1 SCHPO
STANDARD;

P07334; Q9P6Q4;
01-APR-1988 (Rel. 07, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-PEB-2003 (Rel. 41, Last annotation update)
28-PEB-2003 (Rel. 41, Last annotation update)
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STRAIN-972
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[2]
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SEQUENCE FROM N.A.
MEDLING=91169281; PubMed=2004705;
Feilotter H., Nurse P., Young P.G.;
Feilotter H., Nurse analysis of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein kinase homologs
Cell 49:569-576(1987).
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Russell P., Nurse
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NCBI_TaxID=4896;
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Nature 415:871-880(2002).

-I- PUNCTION: THIS PROTEIN, A DOSE-DEPENDENT MITOTIC INDUCER, APPEARS TO FUNCTION AS A NEGATIVE REGULATOR OF MITOSIS INHIBITOR WEEL BY PHOSPHORYLATING AND INACTIVATING IT.

-I- SIMILARITY; BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
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SMART; SM00220; S TKc; 1.
PROSITE; PS00100; PROTEIN_KINASE_ATP; 1
PROSITE; PS00108; PROTEIN_KINASE_DOM; 1
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSSP, Q63450; 1A06.

Genebb Spombe; SPAC644.06c; ...

InterPro; IPR000719; Prot kinase.

InterPro; IPR002290; Ser_Thr_pkinase.

InterPro; IPR001245; Tyr_pkinase.

Pfam; PF000669; pkinase; IPR001245; Pfam; PF00069; pkinase; IPR0175; PR00109; TYRKINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
15-JUL-1999 (Rel. 38, Created)
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                                              STANDARD;
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ATP (BY SIMILARITY).
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A -> I (IN REF. 1).
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Mismatches
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                     RA COllins M., Connor R., Cronhor R., Cronhor R., Collins M., Connor R., Cronhor R., Harris D., Hidalgo J., Hodgson G., RA Holroyd S., Hornsby T., Howarth S., Huckle S.J., Hunt S., Jägels K., Jänes M., Leather S., McDonald S., McLean J., RA Jänes K., Jones M., Leather S., McDonald S., McLean J., RA Jänes K., Jones M., Leather S., McDonald S., McLean J., RA Jänes K., Jones M., Leather S., McDonald S., McLean J., RA McDonald S., McLean J., Season D., Guail M.A., Rabbinowitsch E., RA Oliver K., O'Neil S., Pearson D., Quail M.A., Rabbinowitsch E., RA Oliver K., O'Neil S., Pearson D., Seger K., Sharp S., Stevens K., Sharp S., Skelton J., Simmonds M., Squares R., Squares S., Stevens K., Sharp S., RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B., Ra Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H., RA Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H., RA Gaffeau A., Cadieu E., Dreano S., Gloux S., Lehaure V., Mottier S., RA Gaffeau A., Cadieu E., Dreano S., Gloux S., Lehaure V., Mottier S., RA Gaffeau A., Cadieu E., Dreano S., Gloux S., Lehaure V., Mottier S., RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M., Baga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J., RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J., RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J., RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J., RA Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J., Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;

"The genome sequence of Schizosaccharomyces pombe.";

RL Nature 415:871-880(2021).

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SPCC74.03C.
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                                                                                                                                                                                                                                         Pfam; PF00069; pkinase; 1.
ProDom; PD000001; Prot_kinase; 1.
SMART; SM00220; S. TKC; 1.
PROSITE; PS00107; PROFIN KINASE ATP;
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Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Schizosaccharomyces pombe (Fission yeast).
Bukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetacese;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                or send an email to license@isb-sib.ch).
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15-SEP-2003 (Rel.
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InterPro; IPR002290; Ser_thr_pkinase.
InterPro; IPR000449; UBA_domain.
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a collaboration

Benito J.,

8

SIMILARITY).

Query Match Best Local Similarity 25.8%; Pred. No. 7.5e-14; Best Local Similarity 25.8%; Pred. No. 7.5e-14; Matches 83; Conservative 54; Mismatches 133; Indels 52; Gaps 11 Oy 52 PPTAPDRATAVATASRLGPYVLLEP-EEGGRAYRALHCETGTEYTCKVYP 100 Db 22 PPEAISKRHIGPYIIRETLGEGSFGKVKLATHYKTQQKVALKFISRQLLKKSD 74 OY 101VQEALAVLEPYARLPPHKHVARPTEVLAGTQLLYAFFTRTHGDMHSLVRSRHRIPE 156 Db 75 MHMRVEREISYLKLLRHPHIIKLYDVITTPTDIVMVIEYAGGELFDYIVEKKRMTE 130 OY 157 PEAAVLFRQMATALAHCHQHGLVLRDLKLCRFVFADRERKKLVLENLEDSCVLTGPDDSL 216 Db 131 DEGRRFPQQIICAIEYCHRHKIVHRDLKPENLLLDDNLNVKIADFGLSNIMTDGN 185 OY 217 WDKHACPAYVGPEILSSRASYSGKAADVWSLGVALFTMLAGHYVFQDSEPVLLFGKIR 274 Db 186 FLKTSCGSPNYAAPEVINGKL-YAGPEVDWSCGIVLYVMLVGRLPFDDBFIPNLFKKVN 244 OY 275 RGAYALPAGLSAPARCLVRCLLRREPAERLTATGILLHPMLRQDPMPLAFTRSHLMEAAQ 334 OY 289 -LPDYLRPMEEVQGSYADSRIV 309

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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10	277.5	14.7	502	N	T02306
11	277	14.6	441	N	E85362
12	277	14.6	511	س ،	A56009
14	274	14.5	513	,	860304
15	273.5	14.5	533	_	A34366
16	273	14.4	504	N	T07415
17	272.5		480	N	A86427
10	271.5	14.4	421	N	E96522
19	271	14.3	431	N	T02496
2 0	271	14.5	5/6) N	/85Tb.
22	270	14.3	512	, ,	T07788
23	269	14.2	542	_	A45025
24	268.5	14.2	593	_	KIZPMN
25	268	14.2	622	_	844859
26	267	14.1	472	N	B90100
27	266	14.1	542	_	A26464
28	266	14.1	589	N	S68470
29	264	14.0	442	N	T48203

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256.5	257.5	258	258	258.5	258.5	259	260.5	260.5	260.5	261.5	261.5	261.5	261.5	263
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3U0270	T03271	T33998	A41361	T50802	T14736	T06107	A38903	A53621	S59941	T40503	851025	860303	T48202	859359
probable procein k Ca2+/calmodulin-de	calcium-dependent	hypothetical prote	serine/threonine-s	eerine/threonine p	probable serine/th	probable serine/th	protein kinase 1 -	[hydroxymethylglut	веrine/threonine-в	protein kinase kin	[hydroxymethylglut	serine/threonine-в	protein kinase AK2	GIN4 protein - yea

ALIGNMENTS

A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-631 < DON>
A; Cross-references: GB:U21392; GB:U22434
A; Cross-references: GB:U21392; GB:U22434
C; Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homo C; Ksupords: ATP; phosphotransferase
P; 61-315/Domain: protein kinase homology < KIN> R;Donohue, P.J.; Alberts, G.F.; Guo, Y.; Winkles, J.A. J. Biol. Chem. 270, 10351-10357, 1995
A;Title: Identification by targeted differential display of an A;Reference number: A57286; MUID:95247749; PMID:7730342
A;Accession: A57286 RESULT 1 A57286 밁 ş ঠ 밁 \$ 밁 밁 probable serine/threonine protein kinase (EC 2.7.1.-) fnk - mouse
C;Species: Mus musculus (house mouse)
C;Date: 01-Dec:1995 #sequence_revision 01-Dec-1995 #text_change 10-Sep-1997
C;Accession: A57286 문 Ś S Best Loc Matches Query Match Local 297 237 YSGKAADVWSLGVALFTMLAGHYPFQDSSPVLLFGKIRRGAYALPAGLSAPARCLVRCLL 296 183 179 VLRDIKICRFVFADRERKKIVLENLEDSCVLTGPDDSLWDKHAC--PAYVGPEILSSRAS 236 123 IVRFSHHFEDADNIYIFLELCSRKSLAHIWKARHTLLEPEVRYYLRQILSGLKYLHQRGI 182 120 VARPTEVLAGTQLLYAFETR-THGDMHSLVRSRHRIPEPEAAVLERQMATALAHCHQHGL 178 66 GRLLGKGGFARCYEATDTESGIAYAVKVIPQSR---VAKPHQREKILNEIELHRDLQHRH 122 78 10 39 PQPRLPPCLLPLSPPTAPDRATAVATAS-RLGPYVLLEPB-------Similarity RASPRDRPSIEQILRHDFFTKGYTPDRLPVS----SCVTVPD RREPAERLTATGILLHPWLRQ----DPMPLAPTRSHLWEAAQVVPD 338 -HGPEADVWSLGCVMYTLLCGSPPPETADLKETYRCIKQVHYTLPASLSLPARQLLAAIL LHRDLKLGNFFITD--NMELKVGDFGLAARLEPPEQR--KKTICGTPNYVAPEVLLRQG- 237 PRP-FPRAAVPSAPPAGPG---PPANASPRSEPEVLAGPRAPDPPGRLITDPLSGRTYTK 65 ----EGG--RAYRALHCPTGTEYTCKVYPVQEALAVLEPYARLP------PHKH 119 Conservative 15.8%; Score 298.5; DB 2; 28.3%; Pred. No. 4.5e-13; tive 48; Mismatches 133; Indels Length 631; immediate early gene en 67; Gapa 77 14

T20941 hypothetical protein F15A2.6 - Caenorhabditis elegans C;Species: Caenorhabditis elegans

201 251 148

261

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RESULT 3
852244
p69Eg3 protein - African clawed frog
c;Species: Xenopus laevis (African clawed frog)
C;Species: Xenopus laevis (African clawed frog)
C;Date: 07-May-1995 #sequence_revision 03-Aug-1995 #text_change 24-May-2001
C;Accession: $52244
R;Roghi, C.; le Guellec, R.; Paris, J.; Couturier, A.; Philippe, M.
submitted to the EMBL Data Library, October 1992
A;Description: Eg3, selected by differential screening encodes a new Xenopus pr
A;Reference number: $52243
A;Accession: $52244
A;Btatus: preliminary
A;Molecule type: mRNA
A;Residues: 1-51 <ROG>
A;Cross-references: EMBL:217205; NID:g609283; PIDN:CAA78913.1; PID:g609284
C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kins
C;Keywords: ATP
F;11-265/Domain: protein kinase ATP-binding motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pubmitted to the EMBL Data Library, March 1996
A;Reference number: Z19349
A;Accession: T20941
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-887 <WIL>
A;Cross-references: EMBL:Z70207; PIDN:CAA94127.1; GSPDB:GN00028; CESP:F15A2.
A;Experimental source: clone F15A2
C;Genetics:
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A, Introns: 32/1,
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                        Query Match
Best Local S
Matches 73
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Gene: CESP:P15A2.6
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62
                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    h 15.8%; Score 298; DB 2; L
Similarity 25.9%; Pred. No. 7.1e-13;
95; Conservative 51; Mismatches 133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VATASRLGPYVL---LEPEEGGRAYRALHCPTGTEYTCKV-----YPVQEALAV 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               M----KLIEHPHVLHLYDVYENKKYLYLLLEHVSGGBLFDYLVRKGRLMSKEARKFFRQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LEPYARLPPHKHVARPTEVLAGTQLLYAFFTR-THGDMHSLVRSRHRIPEPEAAVLFRQM 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TRIVLRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REVVLYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VI PGEDS I DPDVLRHMNCLGCPKDKQKL I NELLS PKHNTEKMVYFLLLDRKRRPAQEDD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AYALPAGLSAPARCLVRCLLRREPAERLTATGILLHPWL----RQDP---MPLAP-TRSH 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ---- GSPHYACPEVIRGE-KYDGRKADVWSCGVILYALLVGALPFDDDNLRNLLEKVKRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WDKHACPAYVGPBILSSRASYSGKAADVWSLGVALPTMLAGHYPPQDSBPVLLFGKIRRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ISALDFCHAHNICHRDLKPENLLLDERNNIKVADFGMASLQVEGSMLETSC----- 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATALAHCHOHGLVLRDLKLCRFVFADRERKK-----LVLEN--LEDSCVLTGPDDSL 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VAQAQYCGPYKLEKTLGKGQTGLVKTGTHCITGRKVAIKIVNKEKLSESVLQKVEREIAI 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63/3; 92/2; 139/2; 189/3; 328/2; 448/2; 516/3;
                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           359
                                          15.5%;
29.9%;
                        48;
                                          Score 292.5; DB 2;
Pred. No. 1.2e-12;
                        Mismatches 102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    #text_change 18-Peb-2000
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                        Indels
                                                          Length
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                                                          651;
                      21;
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                      Gaps
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                                                                                                                                                     kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        351
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                    7;
                                                                                                                                                                                                                                                                                         protein
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C; Function
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 4

$72513

FOG2 protein - yeast (Kluyveromyces marxianus var. lactis)

C;Species: Kluyveromyces marxianus var. lactis, Candida sphaerica

C;Date: 29-Jan-1998 #sequence_revision 06-Feb-1998 #taxt_change 0'

C;Accession: $72513
RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Title: FOG1 and FOG2 genes, required for A; Reference number: $72513; MUID: 96171514; A; Accession: $72513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Goffrini, P.; Ficarelli, A.;
Curr. Genet. 29, 316-326, 1996
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Best Local S
Matches 88
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                        310
                                                                                                                                 260 ASLIKOMLIVNPVNRITVHEIMODEWFKVDLPDYLVPAESTHOENS
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                                                        EDGGPSVPL
                                                                                            BEGDREVVL 356
                                                                                                                                                                   RCLVRCLLRREPAERLTATGILLHPWLRQD-PMPLAPTRSHLWEAAQVVPDGLGLDEARE 347
                                                                                                                                                                                                                                              EILSSRASYSGKAADVWSLGVALFTMLAGHYPFQDSBPVLLFGKIRRGAYALPAGLSAPA 288
                                                                                                                                                                                                                                                                                  DYCHRHKIVHRDLKPENLLLDEHLNVKIADFGL--SNIMT---DGNPLKTSCGSPNYAAP
                                                                                                                                                                                                                                                                                                                       AHCHQHGLVLRDLKLCRFVFADRERKKLVLENLEDSCVLTGPDDSLWDKHAC--PAYVGP 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATASRLGPYVLLEP-EEG--GRAYRALHCPTGTEYTCKVYPVQBALAVLE-----P
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                                                                                                                                                                                                          EVISGKL-YAGPEVDVWSSGVILYVWLCRRLPFDDESIPVLFKNISNGVYTIPNPLSQGA
                                                                                                                                                                                                                                                                                                                                                               YLRLLRHPHIIKLYDVIKSKDBIIMVIBYAGNBLFDYIVQRDKMPBQBARRFFQQIISAV
                                                                                                                                                                                                                                                                                                                                                                                                                                            AQGQHIGKYQIIKTLGEGSFGKVKLAYHISTGQKVALKIIN-KKVLAKSDMQGRIEREIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KLI-----DFGLCAKPKGGL-DYHLMTCCGSPAYAAPELIQGKA-YIGSBADIWSMGVLM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TR-THGDMHSLVRSRHRIPEPEAAVLFROMATALAHCHOHGLVLRDLKLCRFVFADRERK 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALHCPTGTEYTCKVYPVQEALAVLEPYARLP-----PHXHVARPTEVLAGTQLLYAFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KLVLENLEDSCVLTGPDDSLWDKH-----ACPAYVGPEILSBRASYSGKAADVWSLGVAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BYCPGGELFDYIIAKDRLTEBBARVFFRQIVSAVAYIHSQGYAHRDLKPENLLIDBDQNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ASHLITGEKVAIKIMD-KESLGDDLPRVKTBIDAMKNLSHQHVCRLYHVIBTPKKIFMVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15.4%; 5c.
/ 28.5%; Pref
                                                      310
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 291; DB 2;
Pred. No. 1.4e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches 138; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kluyveromyces lactis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 602;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  activation of glucose-r
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     32;
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gene

ехргевв

BSKT

259

200

85

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probable serine/threonine-specific protein kinase N/Alternate names: SNF1-related protein kinase C/Species: Cucumis sativus (cucumber) C/Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 C/Accession: T10449 #sequence_revision 16-Jul-1999 R/Gumpel, N.J.
                                                                                                                                                    RESULT
T10449
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G/Senetics:
A/Genetics:
A/Genetics:
A/Genetics:
A/Gross-references: SGD:S0001584; MIPS:YKL101w
A/Cross-references: SGD:S0001584; MIPS:YKL101w
A/Map position: IIL

G/Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homol C/Superfamily: unassigned Ser/Thr or Tyr-specific protein kinase homol C/Keywords: ATP; P-loop; purine nucleotide binding; serine/threonine-specific protein k F/79-369/Domain: protein kinase homology <KIN>
F/79-86/Region: protein kinase ATP-binding motif
F/85/Binding site: ATP/GTP (Lys) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A,Residues: 1-1518 <CHR>
A,Cross-references: EMBL:Z28101; NID:g486168; PIDN:CAA81941.1;
A,Experimental source: strain S288C
A,Pallier, C.; Valens, M.; Puzos, V.; Fukuhara, H.; Cheret, G.; Yeast 9, 1149-1155, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       grobable purine nucleotide-binding protein YKL101w - yeast (Saccharomyces cerevisiae)
N/Altornate names: protein YKL453
C/Species: Saccharomyces cerevisiae
C/Species: Saccharomyces cerevisiae
C/Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 24-Sep-1999
C/Accession: 837928; S39084
C/Accession: 837928; S39084
R/Cheret, G./ Fukuhara, H./ Bolotin-Fukuhara, M./ Daignan-Fornier, B./ Pallier, C./ Protein G./ Pukuhara, H./ Bolotin-Fukuhara, M./ Daignan-Fornier, B./
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A/Molecule type: DNA
A/Residues: 1-1518 <PAL>
A/Cross-references: EMBL:X
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A;Accession: 837928
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Best Local :
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|Experimental source: strain S288C
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26.7%;
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Pred. No. 7.3e-12;
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1994
                                                   #text_change
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A;Description: EC 2.7.1.-; serine/threonine-specific protein kinase AKIN11 (validated, complements SNF1 mutations in yeast C;Superfamily; AMP-activated protein kinase; protein kinase homology
                                                                                                                                                                                                                                                                                                                                                                 R;Bhalerao, R.P.; Salchert, K.; Bako, L.; Okresz, L.; Szabados, L.; Muranaka, Proc. Natl. Acad. Sci. U.S.A. 96, 5322-7, 1999
A;Title: Regulatory interaction of PRLI WD protein with Arabidopsis SNP1-like A;Reference number: Z25116; MUID:99238528; PMID:10220464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          serine/threonine-specific protein kinase (EC 2.7.1.-) AKIN11 [validated] - Arabidopsis N,Alternate names: SNF1 protein kinase omolog AKIN11 C;Species: Arabidopsis thaliana (mouse-ear cress) C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 24-Oct-2000 #sequence_revision 24-Oct-2000 #text_change 03-Nov-2000
                                                                                     C;Superfamily: AMP-activated protein kinase; protein kinase homology C;Keywords: ATP; phosphotransferase; serine/threonine-specific prote
                                                                                                                                                                                                                                           A;Cross-references: EMBL:X99279; PIDN:CAA67671
A;Experimental source: cultivar Columbia
                                                                                                                                                                                                                                                               A;Residues: 1-512 <BHA>
A;Cross-references: EMBI
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28.6%;
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28.3%; Pred. No. 3.4e-12;
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                        3.5e-12
                                            DB 2;
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Mach

80 GRAYRALHCPTGTEYTCKVY---

PVQEALAVLEPYARLPPHKHVARPTEVL

Tue

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RESULT 6

UC1446

UC1446

Berline/threonine-specific protein kinase (EC 2.7.1.-) AK21 - Arabel Arabethreonine-specific protein kinase SNF1 homolog

NyAlternate names: protein kinase SNF1 homolog

C.Species: Arabidopsis thallana (mouse-ear cress)

C.Species: Arabidopsis thallana (mouse-ear cress)

C.Species: 30-Sep_1993 #seguence revision 30-Sep_1993 #text_change

C.Accession: UC1446; S58266; $66334

C.Accession: UC1446; S58266; $66334
                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: DNA
A;Residues: 144-198 <TH2>
A;Cross-references: EMBL:X86966; NID:g928909; PIDN:CAA60529.1; PID:g928910
C;Comment: This enzyme plays an important role in a signal transduction case C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;LeGuen, L.; Thomas, M.; Bianchi, M.; Halford, N.G.; Kreis, M. gene 120, 249-254, 1992
A;Title: Structure and expression of a gene from Arabidopsis thaliana encoding A;Reference number: JC1446; MUID:93013041; PMID:1339373
A;Accession: JC1446
                                                                                                  A)Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threoning (38uperfamily: AMP-activated protein kinase; protein kinase homology C;Keywords: ATP; magnesium; phosphotransferase; serine/threonine-specific protein kinase F;17-271/Domain: protein kinase homology <KIN>F;17-271/Domain: protein kinase homology <KIN>F;25-33/Region: protein kinase homology omotif F;48,67;147,144/Active site: Lys, Glu, Asp, Lys #status predicted F;147,151/Binding site: magnesium (Asn, Asp) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: DNA
A;Residues: 144-198 <THU>
A;Residues: 144-198 <THU>
A;Crose-references: EMBL:X86966; NID:g928909; PIDN:CAA60529.1;
A;Thuemmler, P.; Kirchner, M.; Teuber, R.; Dittrich, P.
Plant Mol. Biol. 29, 551-565, 1995
A;Title: Differential accumulation of the transcripts of 22 nov
A;Reference number: S66314; MUID:96123233; PMID:8534852
A;Accession: S66334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: GB:M93023; NID:g166599; PIDN:AAA32736.1; R;Thuemmler, P.; Kirchner, M.; Teuber, R.; Dittrich, P. gubmitted to the EMBL Data Library, May 1995
A;Description: Differential accumulation of the transcripts capacity of the complex: S58256
A;Reference number: S58256
A;Accession: S58266
A;Status: preliminary
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                                                                                                                                                                                                                                                                                                                    A;Gene: AKin10; AK21
A;Introne: 64/1; 125/3; 186/3; 230/3; 292/3; 322/3; 350/3; 396/3; 475/3
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A; Residues: 1-512 < LEG>
Query Match
Best Local Similarity
Matches 87; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NLLLDSRCNIKIADFGLSNVMRDGHFLKTSC----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGTQLLYAFFTRT-HGDMHSLVRSRHRIFEPEAAVLFRQMATALAHCHQHGLVLRDLK-- 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SANG
G
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  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  358
14.9%; Score 281; DB 1;
28.7%; Pred. No. 5.6e-12;
ive 46; Mismatches 118
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                                                  Length 512;
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RESULT 10 T02306

probable protein kinase (imported) - Arabidopsis thaliana N;Alternate names: hypothetical protein F13P17.2

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serine/threonine-specific protein kinase SPK-1 (EC 2.7.1.-) - soybean G;Species: Glycine max (soybean) C;Date: 28-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 18-Jun-1999 C;Accession: S56719 R;Shin, P.G.; Yoon, H.W.; Jeong, Y.H.; Bahk, J.D.; Hong, J.C.; Cho, M.J. submitted to the EMBL Data Library, January 1993 A;Description: Cloning of a novel protein serine/threonine kinase cDNA from A;Reference number: S56719
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S56719
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F;11-19/Region:
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A;Residues: 1-339 <BHI:
A;Residues: 1-339 <BHI:
A;Residues: 1-339 <BHI:
A;Cross-references: EMBI:L01453; NID:g169990; PIDN:AAA33979.1; PID:g169991
A;Cross-references: EMBI:L01453; NID:g169990; PIDN:AAA33979.1; PID:g169991
C;Superfamily: kinase-related transforming protein; protein kinase homology
C;Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase; P;3-261/Domain: protein kinase homology <KIN-
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272
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                                                                                                                                                                                                                                                                  167 ATALAHCHQHGLVLRDLKL------
                                                                                                                                                                                                                                                                                                                                                  117 HKHVARPTEVLAGTQLLYAFPTRTH------GDMHSLVRSRHRIPBPBAAVLFRQM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              87
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NLLLDSKCNVKIADFGLSNIMRDGHFLKTSC-----
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                                                                                                                                                                                                                               ISGVSYCHSMQICHRDLKLENTLLDGNPAPRLKICDFGFS----KSALLHSQPKSTVGT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YAGPEVDVWSCGVILYALLCGTLPFDDENIPNLFKKIKGGIYTLPSHLSPGARDLIPRML
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PERRGYVDHKRTQPSQSVEETMRIIQEARTKIHTGEQAGTGTSDAVHGDRANEE
                                                                                                                                                                                         PDDSLWDKHACPAYVGPEILSSRASYSGKAADVWSLGVALFTWLAGHYPFQDSEPVLLF-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein kinase ATP-binding motif
                                                                                                           -GKIRRGAYALP--AGLSAPARCLVRCLLRRBPABRLTATGILLHPWLRQD-PMPL--
                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                         14.8%;
                                                                                                                                                  35;
                                                                                                                                                                                                                                                                                                                                                                                                         Score 280; DB 2;
Pred. No. 4.2e-12;
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                                    APTRSHLWEAAQV-VPDGLGLDBARBB 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -QAHLPRYLAVPPPDTVQQAKKIDEEILQEVI
                                                                                                                                                                                                                                                                    ---- CREVEADRERKKLVLENLEDSCVLTG
                                                                                                                                                                                                                                                                                                                                                                                                                             Length 339;
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                                                                                                                                                                                                                                                                                                                                                                                        98;
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hypothetical protein AT4g30960 [imported] - Arabidopsis thaliana (Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 02-Mar-2001 C;Accession: E85362 R;anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold. Nature 402, 769-777, 1999
A;Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana. A;Reference number: A85001; MUID:20083488; PMID:10617198
A;Accession: E85362
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-441 <STO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change 1
C;Accession: 702306; D84753
R;Rounsley, S;D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, submitted to the BMBL Data Library, July 1998
A;Description: Arabidopsis thaliana chromosome II BAC F13P17 gence A;Recession: 702306
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
                                                                                                                                                                                                                                                               RESULT
E85362
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A;Experimentel source: cultivar Columbia
R;Lin, X.; Kaul, S.; Rounsley, S.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffet, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, L.
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: D84753
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C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases;
P;55-311/Domain: protein kinase homology <KIN>
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A, Residues: 1-502 <STO>
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Pred. No. 9.6e-12;
9; Mismatches 193;
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A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threon C;Superfamily: AMP-activated protein kinase; protein kinase homology C;Keywords: ATP; magnesium; phosphotransferase; serine/threonine-specific protein kinase F;17-271/Domain: protein kinase homology <KIN-F;271/Domain: protein kinase homology <KIN-F;25-33/Region: protein kinase ATP-binding motif F;48,67,142/AActive site: Lys, Glu, Asp, Lys #status predicted F;147,151/Binding site: magnesium (Asn, Asp) #status predicted
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A; Residues: 1-511 < MUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R; Muranaka, T.; Banno, H.; Machida, Mol. Cell. Biol. 14, 2958-2965, 199
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A;Map position: 4
C;Superfamily: unassigned
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C;Genetics:
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                                                                                        ETPSDIYVVMBYVKSGELFDYIVEKGRLQBDEARKFFQQIISGVBYCHRNMVVHRDLKPB
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Pred. No. 1.1e-11;
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YSGKAADVWSLGVALFTMLAGHYPFQDSEPVLLFGKIRRGAYALPAGLSAPARCLVRCLL

OY 159 AAVLFROMATALAHCHOHGLVLRDLKLCRFVFADRERKKLVLENLEDSCVLTGFDDSLMD 218	108 94	# # U	, 177, 179/Active site: Lys, Glu, , 177, 179/Active site: Lys, Glu, 16/Binding site: magnesium (Asn, nding site: phosphate (Thr) (co	atalyzes the forms for expression of for expression of MP-activated prote autophosphorylati autophosphorylati kinase ho	A;Reterence number: 803044 A;Reteleston: 869644 A;Rolecule type: DNA A;Rolecule type: DNA A;Rolecule type: DNA A,Rolecule type: DNA A,Rolecule type: DNA A,Rolecule type: DNA A,Rolecule type: DNA C,Genetice: EMBL:U33050; NID:g927726; PIDN:AAB64904.1; PID:g927732; GSPDB:GN0000 C;Genetice: EMBL:U33050; NID:g927726; PIDN:AAB64904.1; PID:g927732; GSPDB:GN0000 C;Genetice: SGD:SNP1; MIPS:YDR477w A,Gene: SGD:SNP1; MIPS:YDR477w A,Gene: SGD:SNP1; MIPS:SO002885; MIPS:YDR477w	A;Accession: A40030 A;Accession: A40030 A;Accession: A40030 A;Accession: A40030 A;Residues: 1-633 <cel> A;Cross-references: EMBL:M13971; NID:g172629; PIDN:AAA35058.1; PID:g172630 R;Dietrich, F.S. R;Dietrich, F.S. submitted to the EMBL Data Library, August 1995 A;Description: The sequence of S. cerevisiae cosmids 9410, 8035, 8166, and 9787.</cel>	C.Species: Saccharomyces cerevisiae C;Date: 20-Aug-1987 #sequence_revision 20-Aug-1987 #text_change 23-Mar-2001 C;Accession: A26030; 869644 R;Celenza, J.L.; Carlson, M. Science 233, 1175-1180, 1986 A;Title: A yeast gene that is essential for release from glucose repression encodes a pt A;Reference number: A26030; MUID:86289463; PMID:3526554	RESULT 13 RESULT 13 A26030 Serine-Chreonine-specific protein kinase (BC 2.7.1) SNP1 - yeast (Saccharomyces cereviserinate names: protein YDR477w	355 VLYG	QY 297 RREPAERLTATGILLHPWLRQDPWPLAPTRSHLWEAAQVVPDGLGLDEARBEEGDREV 354	Db 193 YAGPEVDVWSCGVILYALLCGTLPFDDENIPNLFKKIKGGMISLPSHLSAGARDLIPRML 252
RESULT 15 A34366 Ca2+/Calmodulin-dependent protein kinase (EC 2.7.1.123) II delta chain - rat Ca2+/Calmodulin-dependent protein kinase II delta chain, various splice fo N;Contains: Ca2+/calmodulin-dependent protein kinase II delta chain, various splice fo C;Species: Rattus norvegicus (Norway rat) C;Date: 08-Jun-1990 #sequence revision 08-Jun-1990 #text_change 11-Jun-1999 C;Accession: A34366; S39023; S39024; S39025; S39026; S39027; C47170 R;Tobimatsu, T.; Pujisawa, H. J. Biol. Chem. 264, 17907-17912, 1989 A;Title: Tissue-specific expression of four types of rat calmodulin-dependent protein	350 GDREVVLYG 358 298 ILREVVNLG 306	Db 189 ISSKL-YAGPEVDVWSCGVVLYALLCGSVPFDDNIPSLFRXIKGGTYILPSYLSDSARD 247 Oy 291 LVRCLLRREPAERLTATGILLHPWLRQD-PMPLAPTRSHLWEAAQVVPDGLGLDEARBEB 349	Qy 176 HGLVLRDLKLCRFVFADRERKKLVLENLEDSCVLTGPDDSLMDKHACPAYVGPEI 230	Query Match 14.5%; Score 274; DB 1; Length 513; Best Local Similarity 31.7%; Pred. No. 1.7e-11; Matches 79; Conservative 42; Mismatches 102; Indels 26; Gaps 7; Qy 117 HKHVARPTEVLAGTQLLYAFFTR-THGDMHSLVRSBHRIPSPBAAVLFRQMATALAHCHQ 175 : : : : : : :	C;Superfamily: AMP-activated protein kinase; protein kinase homology C;Superfamily: AMP-activated protein kinase; pertein kinase homology C;Keywords: ATP; magnesium; phosphotransferase; serine/threonine-specific protein kinase homology <kin>F;15-272/Domain: protein kinase homology <kin>F;23-31/Region: protein kinase ATP-binding motif F;24-31/Region: protein kinase ATP-binding motif F;46,65,143,145/Active site: Lys, Glu, Asp, Lys #status predicted F;148,152/Binding site: magnesium (Asn, Asp) #status predicted</kin></kin>	A; Reterence number: 824578 A; Accession: 824579 A; Status: preliminary A; Molecule type: mRNA A; Residues: 1-61, 'A', '63-513 <ha2> A; Residues: 1-61, 'A', '63-513 <ha2> A; Cross-references: EMBL: X65604; NID: g18933; PIDN: CAA46554.1; PID: g18934 C; Punction: C; Punction:</ha2></ha2>	A, Accession: 860304 A, Status: preliminary A, Status: preliminary A, Molecule type: mRNA A, Residues: 1-513 <hal> A, Cross-references: EMBL: X65604 R, Halford, N.G. submitted to the EMBL Data Library, April 1992</hal>	C;bpecies: Hordeum vulgate (warley) C;Date: 19-Mar-1997 #sequence_revision 15-Aug-1997 #text_change 11-Jun-1999 C;Accession: S60304; S24579 R;Halford, N.G.; Vicente-Carbajosa, J.; Sabelli, P.A.; Shewry, P.R.; Hannappel, U.; Kr Plant J. 2, 791-797, 1992 Plant J. 2, 791-797, 1992 A;Title: Molecular analyses of a barley multigene family homologous to the yeast prote A;Reference number: S60303; MUID:93258420; PMID:1302632	-		Qy 336 VPDGLGLDEAREEEGD 351

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A, Reference number: A3.
A, Accession: A34366
A, Status: preliminary
A, Molecula
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A;Residues: 314-349,364-368 <SCH>
A;Residues: 314-349,364-368 <SCH>
A;Residues: 314-349,364-368 <NID:g349086
A;Experimental source: skeletal muscle
A;Experimental source: skeletal muscle
A;Note: sequence extracted from NCBI backbone (NCBIN:134450, NCBIP:134453)
C;Complex: heteromultimer composed of 10-12 alpha, beta, gamma, and delta
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A;Molecule type: mRNA
A;Rolecule type: mRNA
A;Residues: 318-349,364-371,504-511,'N' <MA5>
A;Residues: 318-349,364-371,504-511,'N' <MA5>
A;Schworer, C.M.; Rothblum, L.I.; Thekkumkara, T.J.; Singer, H.A.
J. Biol. Chem. 269, 14443-14449, 1993
J. Biol. Chem. 269, 14443-14449, 1993
A;Title: Identification of novel isoforms of the delta subunit of Ca2+/calmodulin-depend A;Reference number: A47170; MUID:93300844; PMID:8390994
A;Accession: C47170
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A;Accession: $39027
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A;Accession: 839024
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EBS Lett. 333, 315-318, 1993
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VTPBAKDLINKMLTINPAKRITASBALKHPWICQ 274
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Sequence 8, Appli
Sequence 102, App
Sequence 1102, App
Sequence 304, App
Sequence 680, App
Sequence 2, Appli
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Sequence 4, Appli
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287 15.2 1518 12 US-10-369-493-2243 Sequence 22.43, A 283.5 15.0 651 10 US-09-974-298-112 Sequence 112, Appl 283.5 15.0 651 12 US-10-354-358-8 Sequence 127, Appl 283.5 15.0 651 12 US-10-295-027-506 Sequence 27, Appl 283.5 15.0 651 12 US-10-399-127 Sequence 327, App 283.5 15.0 651 12 US-10-399-127 Sequence 127, App 283.5 15.0 651 12 US-10-399-3864 Sequence 127, App 283.5 15.0 651 12 US-10-399-3864 Sequence 127, App 283.5 15.0 651 12 US-10-399-3864 Sequence 127, App 284.5 14.8 420 12 US-10-39-3864 Sequence 27, Appli 274.5 14.5 633 10 US-09-824-735-3 Sequence 2, Appli 274.5 14.5 668 14 US-09-824-735-3 Sequence 2, Appli 274.5 14.5 668 14 US-10-369-493-1696 Sequence 2, Appli 273.5 14.5 668 15 US-10-195-071-2 Sequence 2, Appli 273.5 14.5 668 15 US-10-195-071-2 Sequence 2, Appli 273.5 14.5 668 15 US-10-283-247-2 Sequence 2, Appli 273.5 14.5 668 15 US-10-283-247-2 Sequence 2, Appli 273.5 14.3 674 10 US-10-283-247-2 Sequence 2, Appli 279.5 14.3 674 10 US-10-283-247-7 Sequence 2, Appli 279.5 14.3 674 10 US-10-283-247-7 Sequence 2, Appli 279.5 14.3 674 12 US-10-283-247-9 Sequence 3, Appli 279.5 14.3 674 12 US-10-369-493-5806 Sequence 2, Appli 279.5 14.3 674 12 US-10-369-493-5806 Sequence 2, Appli 279.5 14.1 499 12 US-10-369-493-5806 Sequence 2, Appli 279.5 14.1 54.6 12 US-10-369-493-5806 Sequence 2, Appli 279.5 14.1 54.6 12 US-10-369-493-5806 Sequence 3, Appli 279.5 14.1 54.6 12 US-10-369-493-5806 Sequence 6, Appli 279.5 14.1 54.6 12 US-10-369-493-5833 Sequence 6, Appli 279.5 14.1 54.6 12 US-10-369-493-5833 Sequence 6, Appli 279.5 14.1 54.6 12 US-10-369-493-5833 Sequence 2, Appli 279.5 14.5 14.1 54.6 12 US-10-369-493-5833 Sequence 2, Appli 279.5 14.5 14.1 54.6 12 US-10-369-493-5533 Sequence 2, Appli 279.5 14.5 14.1 54.6 12 US-10-369-493-5533 Sequence 2, Appli 279.5 14.5 14.6 14.1 14.1 14.1 14.1 14.1 14.1 14.1
2 1518 12 US-10-369-493-22243 Sequence 20 651 10 US-09-870-937-10 Sequence 10, 651 11 US-10-354-358-8 Sequence 10, 651 12 US-10-354-358-8 Sequence 8, 651 12 US-10-295-027-506 Sequence 8, 651 12 US-10-295-027-506 Sequence 17, 651 12 US-10-13-999-127 Sequence 3, 651 12 US-10-369-493-3864 Sequence 17, 651 12 US-10-369-493-364 Sequence 2, 661 12 US-10-369-493-1696 Sequence 3, 674 15 US-10-283-247-2 Sequence 2, 668 15 US-10-283-247-2 Sequence 2, 668 15 US-10-283-247-2 Sequence 2, 664 12 US-10-283-247-2 Sequence 1, 674 15 US-10-283-247-7 Sequence 2, 674 15 US-10-283-247-7 Sequence 3, 674 15 US-10-283-247-7 Sequence 2, 674 15 US-10-369-493-5806 Sequence 2, 674 15 US-10-369-493-5806 Sequence 2, 674 15 US-10-369-493-5806 Sequence 2, 675 15 US-10-369-493-5806 Sequence 2, 676 172 US-10-369-493-2533 Sequence 2, 677 18 US-10-369-493-253 Sequence 2, 677
12 US-10-369-493-2243 Sequence 29 9 US-09-870-937-10 Sequence 10, 10 US-09-974-298-112 Sequence 10, 10 US-09-974-298-112 Sequence 10, 10 US-09-974-298-112 Sequence 8, 12 US-10-369-493-3864 Sequence 3, 12 US-10-369-493-386 Sequence 3, 12 US-09-824-735-2 Sequence 2, 12 US-09-824-735-2 Sequence 3, 12 US-09-824-735-2 Sequence 3, 12 US-09-824-735-2 Sequence 2, 12 US-10-195-071-2 Sequence 2, 13 US-10-195-071-2 Sequence 2, 15 US-10-283-247-7 Sequence 2, 15 US-10-283-247-7 Sequence 2, 15 US-10-283-247-7 Sequence 2, 15 US-10-283-247-8 Sequence 2, 16 US-10-283-247-8 Sequence 2, 17 US-10-283-247-8 Sequence 2, 18 US-10-283-247-8 Sequence 3, 18 US-09-820-790-4 Sequence 3, 18 US-09-820-790-4 Sequence 2, 18 US-10-369-493-1700 Sequence 2, 18 US-10-369-493-1700 Sequence 2, 18 US-10-369-493-1700 Sequence 2, 18 US-10-369-493-2533
US-10-369-493-22243 US-09-870-937-10 US-09-974-298-112 US-10-295-358-3 US-10-295-027-506 US-10-295-027-506 US-10-173-999-127 US-09-867-550-1772 US-09-8624-735-2 US-09-8624-735-2 US-09-8624-735-3 US-09-8624-735-2 US-09-8624-735-2 US-09-8624-735-2 US-09-8624-735-2 US-09-8624-735-2 US-09-8624-735-2 US-09-8624-735-2 US-09-8624-735-2 US-10-369-493-1696 US-10-195-071-2 US-10-195-071-2 US-10-283-247-7 US-10-283-247-7 US-10-283-247-7 US-10-283-247-7 US-10-283-247-7 US-10-283-247-7 US-10-369-493-5806 US-10-369-493-5806 US-10-369-493-1700 US-10-369-493-1700 US-10-369-493-1533 US-09-862-187-91 US-10-369-493-2533 US-09-863-187-91 US-10-231-913-118 US-09-863-187-91 US-10-231-913-118 Sequence 25
S-10-369-493-22243 Sequence 22 S-09-870-937-10 Sequence 10 Sequence 21 Sequence 22 Sequence 23 Sequence 23 Sequence 24 Sequence 24 Sequence 25 Sequence 26 S-10-195-071-2 Sequence 27 S-10-195-071-2 Sequence 28 S-10-283-247-9 S-10-283-247-9 S-10-283-247-9 S-10-283-247-9 S-10-283-247-9 S-10-283-247-9 S-10-283-247-9 S-10-283-247-9 S-10-283-247-9 Sequence 28 S-10-369-493-5806 Sequence 28 S-10-369-493-1700 Sequence 27 S-10-116-326-6 S-10-369-493-2533 Sequence 27 Sequence 28 S-10-369-493-1700 Sequence 27 S-10-369-493-2533 Sequence 27 Sequence 27 Sequence 28 S-10-369-493-2533 Sequence 27 Sequence 27 Sequence 27 Sequence 27 Sequence 27 Sequence 28 S-10-369-493-1700 Sequence 27 S-10-369-493-1700 Sequence 27 S-10-369-493-1700 Sequence 27 S-10-369-493-1700 Sequence 27 S-10-369-493-1701 Sequence 27 Sequence 27 S-10-369-493-1701 Sequence 27 Sequence 28 Sequence 28 Sequence 29 Sequence 29 Sequence 29 Sequence 29 Sequence 29 Sequence 20 Sequenc
1102 1002 1002 1002 1003 1003 1003 1003

ALIGNMENTS

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APPLICANT: Meyers, Rachel
APPLICANT: Meyers, Rachel
APPLICANT: Williamson, Mark
APPLICANT: Williamson, Mark
ITILE OF INVENTION: NO. US20020034780Alel Human Protein Kinases and Uses
ITILE OF INVENTION: Therefor
FILE REFERENCE: 35800,720996
CURRENT FILING DATE: 2001-03-06
PRIOR APPLICATION NUMBER: 06/182,059
PRIOR APPLICATION NUMBER: 06/182,059
PRIOR FILING DATE: 2000-02-11
PRIOR APPLICATION NUMBER: 09/659,287
PRIOR FILING DATE: 2000-09-12
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PRATSEQ for Windows Version 4.0
SEQ ID NO 8
LENGTH: 358
TYPE: PRI
ORGANISM: Homo sapiens
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Best Local Similarity 99.7%;
Matches 357; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 8, Application US/09799875 Patent No. US20020034780A1 GENERAL INFORMATION:
121 ARPTEVLAGTQLLYAFFTRTHGDMHSLVRSRHRIPEPEAAVLFRQMATALAHCHQHGLVL 180
                                                                   61 AVATASRIGPYVLLEPEEGGRAYRALHCPTGTEYTCKVYPVQBALAVLEPYARLPPHKHV 120
                                                                                                                                                                  1 MRATPLAAPAGSLSRKKRLELDDNLDTERPVQKRARSGPQPRLPPCLLPLSPPTAPDRAT
                                           AVATASRLGPYVLLEPEEGGRAYQALHCPTGTEYTCKVYPVQEALAVLEPYARLPPHKHV
                                                                                                                                       MRATPLAAPAGSLSRKKRLELDDNLDTERPVQKRARSGPQPRLPPCLLPLSPPTAPDRAT
                                                                                                                                                                                                                            Score 1887; DB 9; Length Pred. No. 2.1e-157; 1; Mismatches 0; Indels
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                                                120
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APPLICANT: Virca, Duke
APPLICANT: Bird, Timothy A.
APPLICANT: Bird, Timothy A.
APPLICANT: Bird, Timothy A.
APPLICANT: Marken, John S.
APPLICANT: Marken, John S.
ITILE OF INVENTION: Human cDNAs Encoding Polypeptides Having Kinase
TITLE OF INVENTION: Functions
FILE REPERENCE: 2877-US
CURRENT APPLICATION NUMBER: US/10/024,828
CURRENT FILING DATE: 2001-12-18
PRIOR APPLICATION NUMBER: US/09/509,902A
PRIOR PILING DATE: 1999-08-03
NUMBER OF SEQ ID NOS: 16
SOPTWARE: Patentin Ver. 2.0
SEQ ID NO
SEQ I
RESULT 3
US-09-925-301-1102
### Sequence 1102, Application US/09925301
### Patent No. US20020052308A1
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US-10-024-828-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local
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317, Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RDLKLCRFVFADRERKKLVLENLEDSCVLTGPDDSLWDKHACPAYVGPBILSSRASYSGK 240
                                                                                                                                                                                                                                                                                                                                                  AADVWSLGVALFTMLAGHYPFQDSEFYLLFGKIRRGAYALPAGLSAPARCLVRCLLRREP 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ARPTEVLAGTQLLYAFFTRTHGDMHSLVRSRHRIPEPEAAVLFRQMATALAHCHQHGLVL 180
                                                                                                                                                                                                                                                                                                                  AADVWSLGVALFTMLAGHYPFQDSEFVLLFGKIRRGAYALPAGLSAPARCLVRCLLRREP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AVATASRLGPYVLLEPEEGGRAYQALHCPTGTBYTCKVYPVQEALAVLEPYARLPPHKHV 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AVATASRLGPYVLLEPEEGGRAYRALHCPTGTEYTCKVYPVQEALAVLEPYARLPPHKHV 120
                                                                                                                                                                                                                                  AERLTATGILLHPWLRQD 318
                                                                                                                                                                                                                                                                                                                                                                                                                                     RDLKLCRFVFADRERKKLVLENLEDSCVLTGFDDSLWDKHACFAYVGFEILSSRASYSGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ARPTEVLAGTQLLYAFFTRTHGDMHSLVRSRHRIPEPEAAVLFRQMATALAHCHQHGLVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MRATPLAAPAGSLSRKKRLELDDNLDTERPVQKRARSGPQPRLPPCLLPLSPPTAPDRAT 102
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99.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 1675; DB 15;
Pred. No. 8.8e-139;
1; Mismatches 0;
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GENERAL INFORMATION:

APPLICANT: ROSEN et al.

TITLE OF INVENTION: Nucleic Acids, Proteins and FILE REPERBNCE: PA106

CURRENT APPLICATION NUMBER: US/09/925,301

CURRENT PILING DATE: 2001-08-10

PRIOR APPLICATION NUMBER: PCT/US00/05882

PRIOR FILING DATE: 2000-03-08

PRIOR PILING DATE: 1999-03-12

NUMBER OF SEQ ID NOS: 1694

SOPTWARE: PATENTIN VEY: 2.0

SEQ ID NO 1102

LENGTH: 233

TYPE: PRT

ORGANISM: Homo Bapiens

US-09-925-301-1102
                                                                                                                                              APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: No. US20030228584A1el Nu
FILE REFERENCE: 21272-045
CURRENT APPLICATION NUMBER: US/10/291,172
CURRENT APPLICATION NUMBER: 09/693,267
PRIOR APPLICATION NUMBER: 09/665,363
PRIOR APPLICATION NUMBER: 09/665,363
PRIOR APPLICATION NUMBER: 09/665,363
PRIOR APPLICATION NUMBER: 09/616,847
PRIOR PILING DATE: 2000-09-19
PRIOR APPLICATION NUMBER: 09/516,193
PRIOR PILING DATE: 2000-06-17
PRIOR APPLICATION NUMBER: 09/574,454
PRIOR APPLICATION NUMBER: 09/574,454
PRIOR APPLICATION NUMBER: 09/574,454
PRIOR APPLICATION NUMBER: 09/519,705
PRIOR APPLICATION NUMBER: 09/519,705
PRIOR APPLICATION NUMBER: 09/519,705
PRIOR PILING DATE: 2000-06-19
PRIOR APPLICATION NUMBER: 09/519,705
PRIOR PILING DATE: 2000-03-07
NUMBER OF SEQ ID NOS: 752
PRIOR PILING DATE: 2000-03-07
                                                                                                            ) ORGANISM: Homo sapiens
US-10-291-172-304
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US-10-291-172-304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 304, Applic Publication No. US20 GENERAL INFORMATION:
     Query Match
Best Local Similarity
Matches 133; Conserv
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o. US20030228584A1
       Conservative
36.0%; Score 681.5; DB 12; 51.8%; Pred. No. 1.1e-51; tive 38; Mismatches 79;
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                                                    Length
                                                       269;
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US-10-291-172-680
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US-10-291-172-680
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PRIOR FILING DATE: 2000-10-20
PRIOR PELICATION NUMBER: 09/665,363
PRIOR PILING DATE: 2000-09-19
PRIOR PELICATION NUMBER: 09/616,847
PRIOR APPLICATION NUMBER: 09/516,847
PRIOR FILING DATE: 2000-07-14
PRIOR PELICATION NUMBER: 09/596,193
PRIOR PILING DATE: 2000-06-17
PRIOR PILING DATE: 2000-06-17
PRIOR PILING DATE: 2000-05-19
PRIOR PILING DATE: 2000-05-19
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PRIOR FILING DATE: 2000-03-07
NUMBER OF SEQ ID NOS: 752
SEQ ID NO 680
LENGTH: 290
TYPE: PRT
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Best Local
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TITLE OF INVENTION: No. U
FILE REFERENCE: 21272-045
                                                                                                                                                                                                                                                                                                                                                               / Match 34.9%; Score 659.5; DB 12; Length 290;
Local Similarity 51.2%; Pred. No. 1e-49;
1e8 127; Conservative 42; Mismatches 78; Indels 1;
                                                                      202
                                                                                           271 GKIRRGAYALPAGLSAPARCLVRCLLRRBPABRLTATGILLHPWLRQDPMPLAPTRSHLW 330
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                                EAAQVVPD 338
TSDQIVPB 268
                                                                                                                                                                                                              RKRLREBEAARLFKQIVSAVAHCHQSAIVLGDLKLRKFVFSTEERTQLRLESLEDTHIMK 141
                                                                  SKIRRGOFCIPEHISPKARCLIRSLLRREPSERLTAPEILLHPWFESVLEP-GYIDSEIG 260
                                                                                                                                                                                                                                                RHRIPEPEAAVLFROMATALAHCHOHGLVLRDLKLCRFVFADRERKKLVLENLEDSCVLT 210
                                                                                                                                                                                                                                                                                      GPPFSLQVFPIKHYQDKIRPYIQLPSHSNITGIVEVILGETKAYVFFEKDFGDMHSYVRS
                                                                                                                                                                                                                                                                                                                          GTEYTCKVYPVQEALAVLEPYARLPPHKHVARPTEVLAGTQLLYAFFTRTHGDMHSLVRS 150
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CURRENT APPLICATION NUMBER: US/10/228,263
CURRENT FILING DATE: 2002-12-04
PRIOR APPLICATION NUMBER: US 60/330,797
PRIOR APPLICATION NUMBER: US 60/314,655
PRIOR APPLICATION NUMBER: US 60/314,655
PRIOR FILING DATE: 2001-08-27
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin version 3.1
SEQ ID NO 2
LENGTH: 206
TYPE: PRT
ORGANISM: Homo sapiens
US-10-228-263-2
APPLICANT: HANZE1, DAVIG K.

APPLICANT: Chen, Menbheng

ITILB OP INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OP INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY

FILE REPERENCE: Acomica-X-1

CURRENT APPLICATION NUMBER: US/09/864,761

CURRENT FILING DATE: 2001-05-23

PRIOR APPLICATION NUMBER: US 60/180,312

PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR APPLICATION NUMBER: US 96/32,366

PRIOR APPLICATION NUMBER: US 99/632,366

PRIOR APPLICATION NUMBER: US 60/236,359

PRIOR APPLICATION NUMBER: US 60/26,359

PRIOR APPLICATION NUMBER: US 60/236,359

PRIOR APPLICATION NUM
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US-09-864-761-45767
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Publication No. US20030099985A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David K.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
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TITLE OF INVENTION: AMPLIFIED GENE INVOLVED IN
FILE REFERENCE: 38002-0034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121
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FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00669
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00665

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US-09-925-301-1367

Sequence 1367, Application US/09925301

Patent No. US20020052308A1

GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and FILE REFERENCE: PA106
CURRENT APPLICATION NUMBER: US/09/925,301
CURRENT APPLICATION NUMBER: PCT/US00/05882
PRIOR APPLICATION NUMBER: PCT/US00/05882
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 2000-03-08
PRIOR FILING DATE: 1999-03-12
PRIOR FILING DATE: 1999-03-12
PRIOR FILING DATE: 1999-03-12
PRIOR FILING DATE: 1999-03-12
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SOFTWARE: Annomax Sequence Listing Engine vers.
SEQ ID NO 45767
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Best Local (
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OTHER INFORMATION: E
OTHER INFORMATION: S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 2001-01-30
APPLICATION NUMBER: US 60/234,687
FILING DATE: 2000-09-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00668
FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 09/608,408 FILING DATE: 2000-06-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: PCT/US01/00670 FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: PCT/US01/00661 FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: PCT/US01/00662
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 09/774,203
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           62
PatentIn Ver.
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77; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RVKLESLEDAYILRGDDDSLSDKHGCPAYVSPEILNTSGSYSGKAADVWSLGVMLYTMLV
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NN: EXPRESSED IN PETAL LIVER, SIGNAL = 0.93

NN: EXPRESSED IN PETACENTA, SIGNAL = 0.59

NN: EXPRESSED IN PLACENTA, SIGNAL = 0.59

NN: EXPRESSED IN ADULT LIVER, SIGNAL = 0.9

NN: EXPRESSED IN BRAIN, SIGNAL = 0.93

NN: EXPRESSED IN LUNG, SIGNAL = 0.96

NN: SYRESSED IN LUNG, SIGNAL = 0.96

NN: SYRESSED IN LUNG, SIGNAL = 0.96

NN: SWISSPROT HIT: 074536, EVALUE 1.00e-18

NN: EST_HUMAN HIT: BE897149.1, EVALUE 2.00e-71
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; Pred. No. 4.6e-28;
15; Mismatches 30
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                                                                                                            ; LENGTH: 373
; TYPE: PRT
; ORGANISM: Homo sapiens
; PRATURE:
; NAMB/KEY: DOMAIN
; LOCATION: (1)..(373)
; OTHER INFORMATION: human FNK mitotic kinase kinase
US-10-026-021-4
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; LOCATION: (152)
; OTHER INFORMATION:
US-09-925-301-1367
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-026-021-4
                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: US 60/309,632
PRIOR FILING DATE: 2001-08-01
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 4
                                                       Best Local
Matches 10
                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4, Application US/10026021 Publication No. US20030027756A1
                                                                     Query Match
Best Local !
                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Hitoshi,
APPLICANT: Demo, Su
APPLICANT: Jenkins,
APPLICANT: Rigel Ph
                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local 9
                                                                                                                                                                                                                                                                                           APPLICANT: Rigel Pharmaceuticals, Inc.
TITLE OF INVENTION: SAK: Modulation of Cellular |
TITLE OF INVENTION: Treatment of Cancer
FILE REFERENCE: 021044-001210US
CURRENT APPLICATION NUMBER: US/10/026,021
CURRENT FILING DATE: 2002-06-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYBE: PRT
ORGANISM: Homo sapic
PRATTURE:
PRATTURE:
NAME/KEY: SITE
LOCATION: (136)
OTHER INPORMATION: X
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LOCATION: (142)
OTHER INFORMATION: :
NAME/KBY: SITE
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OTHER INFORMATION:
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11 RPFORTANATAPPAGEGE--PESALRGPELEMLAGLETSDEGRLITDERSGRTYLKGRLL
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                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                          RPVQKRAR-----SGPQPRLPPCL------LPLSPP----TAPDRATAVATASRL
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                                                       48;
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Pred. No. 2.9e
0; Mismatches
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                                                    Score 304.5; DB 1
Pred. No. 2.1e-18;
8; Mismatches 134
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.9e-23;
                                                                                DB 15;
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                                                                                                                            domain
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APELICANT: RUGOLPH-Owen, Laura A.
APPLICANT: RUGOLPH-Owen, Laura A.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
TITLE OF INVENTION: CANCER USING 140, 1470, 1686, 2089, 2427, 3702, 5891, 6428,
TITLE OF INVENTION: 7161, 7660, 25641, 69583, 49663, 8897, 1682, 17667, 9235,
TITLE OF INVENTION: 3703, 14171, 10359, 1660, 1450, 1894, 2088, 32427, 2160,
TITLE OF INVENTION: 8950, 2100, 9288, 64698, 10480, 2089, 33230, 1586, 9943,
TITLE OF INVENTION: 16334, 68862, 9011, 14031, 6178, 21225, 1420, 4469,
TITLE OF INVENTION: 16334, 68862, 9011, 14031, 6178, 21225, 1420, 32236, 2099,
TITLE OF INVENTION: 2150, 26583, 2784, 8941, 9811, 27444, 50566 OR 66428 MOLECULES
FILE REPERENCE: MPIO2-020PIRNOMNIM
CURRENT PAPLICATION NUMBER: US 60/353,600
PRIOR APPLICATION NUMBER: US 60/354,358
CURRENT PILING DATE: 2002-01-31
PRIOR APPLICATION NUMBER: US 60/371,075
PRIOR PILING DATE: 2002-04-10
PRIOR APPLICATION NUMBER: US 60/371,507
PRIOR PILING DATE: 2002-04-16
PRIOR APPLICATION NUMBER: US 60/372,984
PRIOR APPLICATION NUMBER: US 60/372,984
PRIOR APPLICATION NUMBER: US 60/374,194
PRIOR APPLICATION NUMBER: US 60/372,984
PRIOR APPLICATION NUMBER: US 60/374,194
PRIOR APPLICATION NUMBER: US 60/372,985
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US-10-354-358-92
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                                                                                     SOPTWARE: PASTSEQ
SEQ ID NO 92
LENGTH: 778
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
APPLICANT:
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: US 60/385,023
PRIOR FILING DATE: 2002-05-31
PRIOR APPLICATION NUMBER: US 60/388,853
PRIOR FILING DATE: 2002-06-14
PRIOR APPLICATION NUMBER: US 60/389,395
PRIOR FILING DATE: 2002-06-17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            178
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                                                                                                                                                                                Application data removed NOS: 122
                                                                                                                                                      for Windows Version 4.0
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/ ORGANISM: homo sapiens
US-10-116-326-2
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US-10-116-326-2
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APPLICANT: Mathur, Brian
APPLICANT: Wathur, Brian
APPLICANT: Friddle, Carl Johan
TITLE OF INVENTION: No. US20030166889A1el Human Kinases and Polynucleotides Encodin
FILE REFERENCE: LEX-0332-USA
CURRENT APPLICATION NUMBER: US/10/116,326
CURRENT FILING DATE: 2002-04-04
PRIOR APPLICATION NUMBER: US 60/282,036
PRIOR APPLICATION NUMBER: US 60/282,036
PRIOR APPLICATION NUMBER: US 60/282,036
PRIOR FILING DATE: 2001-04-06
NUMBER OF SEQ ID NOS: 6
SOPTWARE: PastSEQ for Windows Version 4.0
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Best Local S
Matches 98
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Best Local
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                                                                                                                                                                                                                                                                                            13
                                                                                                                                                                                                                                                                                                                                 44 PPCLLPLSPPTAPDRATAVATASRIGPYVL---LEPEEGGRAYRALHCPTGTEYTCKV--
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                                                                                                                                                                                                                                                                                                                                                                               98;
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98; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
VLLFGKIRRGAYALPAGLSAPARCLVRCLLRREPAERLTATGILLHPWL---RQDPMPL-
                                       QVG--DSLLET-SCGSPHYACPEVIKGE-KYDGRRADMWSCGVILPALLVGALPPDDDNL
                                                                                                                      VKKGRLTPKEARKPFROIVSALDFCHSYSICHRDLKPENLLL--DEKNNIRIADFGMASL
                                                                                                                                                               RSRHRIPEPEAAVLFROMATALAHCHOHGLVLRDLKLCRFVFADRERKKLVLENLEDSCV
                                                                                                                                                                                                                                                                                          PAYHLPHPHPHPPQHAQYV-----GPYRLBKTLGKGQTGLVKLGVHCITGQKVAIKIVN
                                                                              LTGPDDSLWDKHAC--PAYVGPEILSSRASYSGKAADVWSLGVALFTMLAGHYPFQDSEP
                                                                                                                                                                                                           REKLSESVLMKVERBIAIL----KLIEHPHVLKLHDVYENKKYLYLVLEHVSGGELFDYL
                                                                                                                                                                                                                                                ------YPVQBALAVLBPYARLPPHKHVARPTBVLAGTQLLYAFFTR-THGDMHSLV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EPAPGRR----VAMRSLPSNGELDPDVLESMASLGCFRDRERLHRELRSEEENQEKMIY 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RQLLSKVKRGVPHMPHFIPPDCQSLLRGMIEVBPEKRLSLEQIQKHPWYLGGKHBPDPCL 296
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                                                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                         ; Score 297.5; DB 12;
; Pred. No. 2.2e-17;
54; Mismatches 143;
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RESULT 12
US-09-769-970-15
US-09-769-970-15
Sequence 15. Application US/09769970
Publication No. US20030170219A1
Publication No. US20030170219A1
GENERAL INFORMATION:
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                                                                                                                                                                                US-09-769-970-15
                                                                                                                  Query Match
Best Local Similarity
Matches 92; Conserv
                                                                                                                                                                                                                                                                                                                TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:

APPLICATION UNMBER: 09/272,796

PILING DATE: <Unknown:

ATTORNEY/AGENT INFORMATION:

NAME: Billings, Lucy J J

REGISTRATION NUMBER: 36,749

REGISTRATION NUMBER: PF-0321 US

TELEPHONE: 415-855-0555

TELEPHONE: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM Comparible
OPERATING SYSTEM: DOS
SOPTWARE: Fast-SEQ for Windows Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/769,970
FILING DATE: 24-Jan-2001
CLASSIFICATION: Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals,
STREET: 3174 Porter Drive
                                                                                                                                                                                            SEQUENCE DESCRIPTION: SEQ ID NO: 15:
                                                                                                                                                                                                                         TOPOLOGY: linear IMMEDIATE SOURCE: LIBRARY: GenBank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN KINASES
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57
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                                                                                LPLSPP----TAPDRATAVATASRLGPYVLLBPEEGG--RAYRALHCPTGTEYTCKVYPV
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SR---VAKPHQREKILNEIELHRDLQHRHIVRFSHHFEDADNIYIFLELCSRKSLAHIWK 113
                            QEALAVLEPYARLP------PHKHVARPTEVLAGTQLLYAFFTR-THGDMHSLVR 149
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                                                          LPTSDPGRLITDPRSGRTYLKGRLLG------KGGPARCYEATDTETGSAYAVKVIPQ 56
                                                                                                                                                                                                                                                                    LENGTH: 607 amino acide
TYPE: amino acid
STRANDEDNESS: eingle
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STATE: CA
                                                                                                                                                                                                              CLONE: 1827450
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                                                                                                                     Conservative
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Hilman, Jennifer L.
Corley, Neil C.
Guegler, Karl G.
Lal, Preeti
Goli, Surya K.
Shah, Purvi
                                                                                                                  15.4%; Score 290.5; DB 12; 29.2%; Pred. No. 6.7e-17; ive 45; Mismatches 129;
                                                                                                                     Indels
                                                                                                                                                  Length 607;
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US-10-204-041-16
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; LENGTH: 607
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-204-041-16
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PRIOR FILING DATE: 2002-05-16
NUMBER OF SEQ ID NOS: 20
SOPTWARE: Patentin version 3.1
SEQ ID NO 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 16, Application US/10204041
Publication No. US20030176443A1
GENERAL INFORMATION:
APPLICANT: STEIN GERLACH, MATTHIAS
APPLICANT: SALASSIDIS, KONSTADINOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 15.4%; Score 290.5; DB 12; Length 607; Best Local Similarity 29.2%; Pred. No. 6.7e-17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: BACHER, GERALD
APPLICANT: MULLER, STEFAN
TITLE OP INVENTION: Pyridylpyrimidine Derivatives as Effective Compounds Against
TITLE OP INVENTION: Infections and Prion Diseases
FILE REFERENCE: AXM-007.1P US
CURRENT APPLICATION NUMBER: US/10/204,041
CURRENT FILING DATE: 2002-08-16
FRIOR APPLICATION NUMBER: EP 01111858.5
PRIOR FILING DATE: 2001-05-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  268 LLFGKIRRGAYALPAGLSAPARCLVRCLLRREPABRLTATGILLHPWLRQ----PPMPLA 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         210 TGPDDSLWDKHAC--PAYVGPBILSSRASYSGKAADVWSLGVALFTMLAGHYPFQDSBPV 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               114 ARHTLLEPEVRYYLRQILSGLKYLHQRGILHRDLKLGNPPIT--BNMBLKVGDFGLAARL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            102 QEALAVLEPYARLP------PHKHVARPTEVLAGTQLLYAPFTR-THGDMHSLVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         48 LPLSPP----TAPDRATAVATASRLGPYVLLEPEEGG--RAYRALHCPTGTEYTCKVYPV 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ETYRCIKQVHYTLPASLSLPARQLLAAILRASPRDRPSIDQILRHDFFTKGYTPDRLPIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BPPEOR -- KKTICGTPNYVAPEVLLROG--HGPEADVWSLGCVMYTLLCGSPPFETADLK 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SRHRIPBPBAAVLFROMATALAHCHOHGLVLRDLKLCRFVFADRBRKKLVLBNLBDSCVL 209
                                                                                                                            STYRCIKOVHYTLPASISLPARQLLAAILRASPRDRPSIDQILRHDPFTKGYTPDRLPIS
                                                                                                                                                                                    LLFGKIRRGAYALPAGLSAPARCLVRCLLRREPABRLTATGILLHPWLRO----DPMPLA 323
                                                                                                                                                                                                                                                      BPPEOR -- KKTICGTPNYVAPEVILROG--HGPBADVWSLGCVMYTLLCGSPPPBTADLK 227
                                                                                                                                                                                                                                                                                                                 TGPDDSLWDKHAC--PAYVGPBILSSRASYSGKAADVWSLGVALFTMLAGHYPFQDSBPV
                                                                                                                                                                                                                                                                                                                                                                                          ARHTLLEPEVRYYLROILSGLKYLHORGILHROLKLGNPFIT--ENMELKVGDFGLAARL 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                        SRHRI PEPEAAVLFROMATALAHCHOHGLVLRDLKLCRFVFADRERKKLVLENLEDSCVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SR---VAKPHOREKILNEIELHRDLOHRHIVRFSHHFEDADNIYIPLELCSRKSLAHIWK 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LPTSDPGRLITDPRSGRTYLKGRLLG------KGGPARCYEATDTETGSAYAVKVIPQ 56
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                                                           PTRSHLWEAAQVVPD 338
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----SCVTVPD 294
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RESULT 15
US-09-801-368-152
APPLICANT: Summers, Eric
TITLE OF INVENTION: Methods for Improving Se-
FILE REFERENCE: 109272.147
FURRENT APPLICATION NUMBER: US/09/801,368
CURRENT FILING DATE: 2001-03-07
PRIOR APPLICATION NUMBER: US 09/487,558
PRIOR APPLICATION NUMBER: US 60/160,587
PRIOR APPLICATION NUMBER: US 60/160,587
PRIOR FILING DATE: 1999-10-20
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US-10-108-580-2
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TITLE OF INVENTION: PLK3 PROTEIN-PROTEIN INTERACTIONS
FILE REPERENCE: PU4458
CURRENT APPLICATION NUMBER: US/10/108,580
CURRENT FILING DATE: 2002-03-28
NUMBER OF SEQ ID NOS: 29
SOFTWARE: Patentin version 3.1
SEQ ID NO 2
LENGTH: 607
                                                                                                                                                                                                                                                                                                                                                                               Sequence 152, Application US/09801368 Patent No. US20020128250A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/10108580 Publication No. US20030077681A1 GENERAL INFORMATION:
                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                            APPLICANT: Busby, APPLICANT: Cali,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 29.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        172
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  102 QEALAVLEPYARLP------PHKHVARPTEVLAGTQLLYAFFTR-THGDMHSLVR 149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            92,
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                                                                                                                                                                                                                                   Hecht, Peter
Holtzman, Doug
Madden, Kevin
Maxon, Mary
Milne, Todd
No. US20020128250Alman,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LLFGKIRRGAYALPAGLSAPARCLVRCLLRREPAERLTATGILLHPWLRQ-----DPMPLA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGPDDSLWDXHAC--PAYVGPEILSSRASYSGKAADVWSLGVALFTMLAGHYPFQDSEPV 267
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                                                                                                                                                                Sherman, Amir
Silva, Jeff
                                                                                                                                                                                                   Royer, John
Salama, Sofie
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i, Brian
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                                                                                                                                Secondary Metabolite Production
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Search completed: January 15, Job time: 40 secs
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; TYPE: PRT
; ORGANIEM: Saccharomyces cerevisiae
US-09-801-368-152
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SOFTWARE: PatentIn version
SEQ ID NO 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 15.2%; Score 287; DB 10; Best Local Similarity 26.7%; Pred. No. 4.5e-16; Matches 86; Conservative 50; Mismatches 128;
                                                                                                                                                    296
                                                                                                                                                                                                                                                                                                        179 LFEVWENKSELYLVLEYVDGGELFDYLVSKGKLPEREAIHYFKQIVEGVSYCHSFNICHR
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                                                                           356 KRITTQBILKHPLIKKYDDLPV 377
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  56 PDRATAVATAS------RLGPYVL---LEPEEGGRAYRALHCPTGTEYTCKVYPVQEAL 105
                                                                                                BRLTATGILLHPWLRQ-DPMPL 322
                                                                                                                                                SDVMSCGIVLFALLTGHLPFNDDNIKKLLLKVQSGKYQMPSNLSSEARDLISKILVIDPE 355
                                                                                                                                                                                 ADVWSLGVALFTMLAGHYPFQDSEPVLLFGKIRRGAYALPAGLSAPARCLVRCLLRREPA 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                            PDSTVSVATKSSKRKSRDTVGPNKLGKTLGKGSSGRVRLAKNMBTGQLAAIKIVPKKKAF
                                                                                                                                                                                                                             DLK-PENLLLDKKNRRIKIADF-GMAALELPNKLLKTSCGSPHYASPBIVMGR-PYHGGP
                                                                                                                                                                                                                                                                  DLKLCRFVFADRERKKLVLENLEDSCVLTGPDDSLWDKHACPAYVGPEILSSRASYSGKA
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                   2004, 15:03:53
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118

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Minimum DB :
Maximum DB :
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Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Run
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence:
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                                                     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq length: 0
seq length: 2000000000
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1: /SIDS1/gcgdata/gei
2: /SIDS1/gcgdata/gei
3: /SIDS1/gcgdata/gei
4: /SIDS1/gcgdata/gei
5: /SIDS1/gcgdata/gei
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1891
1 MRATPLAAPAGSLSRKKRLE.....GLGLDEAREBEGDREVVLYG 358
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                                                                                                                                                                | SIDS1/gcgdata/geneseq/geneseqp-emb1/AA198.DAT:*
| SIDS1/gcgdata/geneseq/geneseqp-emb1/AA199.DAT:*
| SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2000.DAT:*
| SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT:*
| SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT:*
| SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT:*
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Copyright (c) 1993 - 2004 Compugen Ltd.
SUMMARIES
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1291.457 Million cell updates/sec
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A thaliana AKIN11	AA017664	23	512	15.0	283	5
ana	AA017663	23	512	15.0	283	4
	ABR40715	24	438	•	283	ü
ean putative	AAB03421	21	438	٠	œ	2
Lung cancer-associ	2	24	651	•	83.	Ξ
Differentially exp	ABU57635	24	651	15.0	83	ö
0175 protei	AAB47857	23	651	•	83.	9
Mouse dominant neg	ABB04769	20	643	٠	•	8
Human dominant neg	ABB04768	20	619	15.0	œ	7
psis thali	AAG36157	21	512	٠	284	8
Cucumie sativus oi	ABR40815	24	504	15.0	284	5
dopsis SN	AAM50578	23	512	•	287	4
Human protein kina	ABP96069	24	1078	•	•	ü
	AA016604	24	754	•	287.5	ະ
n PRK p	AAE34495	24	607		290.5	=
n	ABR40719	24	523	15.4	291	ŏ
п	AAB03425	21	523	15.4	291	8
	ABG16826	22	605		291.5	8
	AAE16271	23	794	•	295	27
an protein kin	AAU03517	22	794	•	295	8
tei	AAG54419	21	327	15.7	297	ទ
Human kinase #1.	ABB98743	24	778	15.7	297.5	24
Zea maya protein f	AAG54418	21	371	16.7	16	ວ
0881	AAB43922	21	153	٠	354	ະ
Human peptide enco	ABG45957	23	138	21.6	408	2
de #1	AAM36904	22	138		408	õ
	AAM76798	22	138	•	408	6
Human brain expres	AAM63978	22	138	٠	408	<u>_</u>
Peptide #10585 enc	ABB43079	22	138	٠	408	5
Human liver peptid	ABG58479	22	138	•	408	2
Drosophila melanog	ABB71379	22	484	•	435	5
Human C8FW protein	ABP96856	24	206	30.6	26	4
l human	AAU28323	22	290	٠	25	ü
=	AAU28135	22	269	•	681.5	2
Human tribbles hom	ABB80975	23	372	39.4	4	Ξ
Human NS protein s	ABB06108	23	278	58.0	1097	6

ALIGNMENTS

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RESULT 1
AAU03509
 WPI; 2001-343950/36.
N-PSDB; AAS06709.
                          Plowman GD,
Flanagan P,
                                                                          24-NOV-1999;
                                                                                            22-NOV-2000; 2000WO-US32085.
                                                                                                                 31-MAY-2001.
                                                                                                                                                                         Human; protein kinase; PTK; STK; cancer; cardiovascular disease; metabolic disorder; immune related disease; neurological disorder; neurodegenerative disorder; inflammatory disorder; infectious diserproductive disorder.
                                                                                                                                                                                                                         Human protein kinase #9
                                                                                                                                                                                                                                                                                   AAU03509 standard; Protein; 358 AA
                                                                                                                                   WO200138503-A2
                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                             12-SEP-2001 (first entry)
                                                                                                                                                                                                                                                                AAU03509;
                                                         (SUGE-) SUGEN INC.
                           Whyte D, Clary D;
                                                                           99US-0167482
                                   Manning G,
                                     Sudarsanam
                                     တ
                                     Martinez
                                                                                                                                                                                    infectious disease;
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Score

Query Match

Length

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ij

Description

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999.6 999.6 999.6 999.6 999.8

358 358 358 393 360 360 323 278

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AAU03509 AAM38908 AAB20326 AAM820369 ABB80976 AAY69157 AAB85791 AAB85791 AAB836579

Human protein kina
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CC AAU03501-AAU03557 represent novel human protein kinases #1-57. The CC novel protein kinases have been identified as members of the tyrosine CC or serine/chreonine kinase (PTK and STM) families. The polymucleotides encoding protein kinases and the polypeptides may be used in the CC encoding protein kinases and treatment of diseases associated with CC inappropriate kinase expression. For example, they may be used to treat CC cancers (e.g. atherosclerosis), metabolic disorders (e.g. diabetes), cc immune related diseases (e.g. rheumatopoietic origin), cardiovascular CC disease (e.g. schizophrenia), neurodegenerative disorders (e.g. diabetes), CC Parkinson's disease), inflammatory disorders (e.g. sathma), infectious CC disease (e.g. HIV) and reproductive disorders (e.g. sathma), infectious CC disease (e.g. polymucleotides encoding protein kinases may be CC used for gene therapy and as DNA probes in diagnostic assays.

CC The protein kinase polypeptides may be used as antigens in the production cof antibodies against the protein kinases and in assays to identify condulators of protein kinase expression and activity.
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Best Local S
Matches 357
                            Human; nootropic; immunosuppressant; cytostatic; gene therapy; cance peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic acids encoding human kinase polypeptides, useful for preventing diagnosing and/or treating e.g. cancer, immune, cardiovascular and neuronal-associated diseases, and microbial infections -
                                                                                                                                Human polypeptide
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                                                                                                                                                                                                                                       standard;
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25-APR-2000;
09-JUL-2000;
19-JUL-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                  the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system disease, such as Alzheiner's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activin/inhibin activity, chemotactic/chemokinetic activity, harmostatic and thrombolytic activity, cancer disgnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and
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19-OCT-2000;
29-NOV-2000;
                                                                                                                                                                                                                                                                               Sequence
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Wang
Zhao
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N-PSDB; AAIS8064.
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Zhou
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             AADVWSLGVALFTMLAGHYPFQDSEPVLLFGKIRRGAYALPAGLSAPARCLVRCLLRREP
                                          RDLKLCRFVFADRERKKLVLENLEDSCVLTGPDDSLWDKHACPAYVGPBILSSRASYSGK
                                                           RDLKLCRFVFADRERKKLVLENLEDSCVLTGPDDSLWDKHACPAYVGPEILSSRASYSGK
                                                                                                                                     AVATASRIGPYVILLEPEEGGRAYQALHCPTGTEYTCRVYPVQEALAVLEPYARLPPHKHV
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7 2000US-0552317.
8 2000US-0598042.
7 2000US-0620312.
8 2000US-0623450.
9 2000US-0623936.
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Wehrman T, X
Goodrich R,
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Xu C,
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                       Novel human protein phosphatase and kinase proteins for diagnosis, treatment and prevention of gastrointestinal, immune system, neurological and cell proliferative disorders -
                                                                                    Yue H,
Lu DAM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protein phosphatase and kinase protein; PPHKP-5; human; gastrointestinal disorder; immune system disorder; cancer; neurological disorder; cell proliferative disorder; cancer;
        Claim 1; Page 88-89; 103pp; English
                                                          WPI; 2001-244811/25
N-PSDB; AAF30480.
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Matches 356
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ABRITATGILLHPWLRQDPMPLAPTRSHLWBAAQVVPDGLGLDBARBBBGDREVVLYG 358
                      ABRLTATGIILLHPWLRQDPWPLAPTRSHLWEAAQVVPDGLGLDEAREEEGDREVVLYG 358
                                                                            AADVWSLGVALFTMLAGHYPFQDSEPVLLFGKIRRGAYALPAGLSAPARCLVRCLLRREP
                                                                                               AADVWSLGVALFTMLAGHYPFQDSEPVLLFGKIRRGAYALPAGLSAPARCLVRCLLRREP
                                                                                                                                                     RDLKLCRFVFADRERKKLVLENLEDSCVLTGPDDSLWDKHACPAYVGPEILSSRASYSGK
                                                                                                                                                                               RDLKLCRFVFADRERKKLVLENLEDSCVLTGPDDSLWDKHACPAYVGPEILSSRASYSGK
                                                                                                                                                                                                                                                                  ARPTEVLAGTQLLYAFFTRTHGDMHSLVRSRHRIPEPEAAVLFRQMATALAHCHQHGLVL
                                                                                                                                                                                                                                                                                                               AVATASRLGPYVLLEPEEGGRAYQALHCPTGTEYTCKVYPVQEALAVLEPYARLPPHKHV
                                                                                                                                                                                                                                                                                                                                     AVATASRLGPYVLLBPBEGGRAYRALHCPTGTBYTCKVYPVQBALAVLBPYARLPPHKHV
                                                                                                                                                                                                                                  ARPTEVLAGTQLLYAPPTRTHGDMHSLVRTRHRIPEPEAAVLPRQMATALAHCHQHGLVL
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Pred. No. 3.9e-171;
2; Mismatches 0;
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RESULT 4 AAM40694

AAM40694 standard; Protein; 393 ጅ

AAM40694;

22-OCT-2001 (first entry)

Human polypeptide SEQ ID NO 5625.

peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinstic; thrombolytic; drug screening; arthritis; inflammation; Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; CNS; WO200153312-A1 Homo sapiens. leukaemia.

26-DEC-2000; 2000WO-US34263

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RESULT 5
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Best Local Sim
Matches 356;
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C.N.S disorders.
The sequer
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25-APR-2000;
09-JUL-2000;
19-JUL-2000;
03-AUG-2000;
14-BEP-2000;
19-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                               the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat disease of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system disease, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tang
Wang
Zhao
                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to human nucleic acids (AAI57798-AAI61369) the encoded polypeptides (AAM38642-AAM42213) with nootropic,
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DB; AAIS9850.
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Zhou
                                                                                                                                                                                        MRATPLAAPAGSLSRKKRLELDDNLDTERPVQKRARSGPQPRLPPCLLPLSPPTAPDRAT
                                                           AERLTATGILLHPWLRQDPMPLAPTRSHLWEAAQVVPDGLGLDEARBEEGDREVVLYG
                                                                                                                                         RDLKLCRFVFADRERKKLVLENLEDSCVLTGPDDSLWDKHACPAYVGPEILSSRASYSGK
                                                                                                                                                          RDLKLCRFVFADRERKKLVLENLEDSCVLTGPDDSLWDKHACPAYVGPEILSSRASYSGK
                                                                                                                                                                                                                                                      AVATASRLGPYVLLBPEEGGRAYRALHCPTGTBYTCKVYPVQEALAVLBPYARLPPHKHV
                                                                                             AADVWSLGVALFTMLAGHYPFQDSEPVLLFGKIRRGAYALPAGLSAPARCLVRCLLRREP
                                                                                                        AADVWSLGVALFTMLAGHYPFQDSEPVLLFGKIRRGAYALFAGI.SAPARCLVRCLLRREP
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                                             AERLTATGILLHPWLRQDPMPLAPTRSHLWEAAQVVPDGLGLDEARBEEGDREVVLYG
                                                                                                                                                                                                                                                                                                                                                                                                                           sequence data
                                                                                                                                                                                                                                                                                                                                                                                         393
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2000US-0552317.

2000US-0598042.

2000US-0620312.

2000US-0653450.

2000US-0653050.

2000US-0693036.

2000US-0727344.
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Wehrman T,
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                                                                                                                                                                                                                                                                                                                                                   99.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                           for this patent did
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               polypeptides, useful
system injuries -
                                                                                                                                                                                                                                                                                                                                       Score 1884; DB 22;
Pred. No. 4.4e-171;
2; Mismatches 0;
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Xu C, Xue
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Zhang
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AVATASRLGPYVLLEPEEGGRAYRALHCPTGTBYTCKVYPVQBALAVLEPYARLPPHKIV

MRATPLAAPAGSLSRKKRLELDDNLDTER PVQKRARSGPQPRLPPCLLPLSPPTAPDRAT MRATPLAAPAGSLSRKKRLELDDNLDTERPVQKRARSGPQPRLPPCLLPLSPPTAPDRAT

Query Match Best Local S Matches 355

Similarity

98.9%;

Score 1870; D Pred. No. 8.5e 3; Mismatches

DB 23; 3.5e-170; hee 0;

Indels Length

2

Gaps

60 60

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Sequence

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The invention provides an isolated human tribbles homologue-1 (htrb-1, CC also known as stress kinase inhibitor procein (SKIP-1)) polypeptide. The christian procein (SKIP-1) polypeptide. The cC htrb polypeptide is useful for inhibiting an AP-1 mediated inflammatory cC signal in a cell. The polypeptide employed in the method is preferably chrb-1, htrb-1 N htrb-1 C, htrb-1 N C, htrb-3, htrb-3 C, or cC htrb-3 N C. It is also useful for providing htrb agonist activation cc signal, an estrogen receptor-mediated signal, or a pMA induced signal, an cC signal, an estrogen receptor-mediated signal, or a pMA induced signal, an cc litth modulators are useful for modulating AP-1 mediated compounds in a cell such as tumor necrosis factor (TNF) c induced inflammatory signal, or an interleukin induced inflammatory compounds e.g. for in screening assays, predictive medicine cc and in therapeutics or prophylactics. The htrb proteins are useful for compounds e.g. for treating and/or preventing diseases caused by abnormal htrb activity, such as rheumacoid arthrits, diabetes, compounds e.g. for treating and/or preventing diseases caused compounds e.g. for treating and/or preventing diseases caused by abnormal htrb activity, such as rheumacoid arthrits, diabetes, compounds in the appetite are useful for antagonizing conformation or autoimmune disorders. The present sequence represents can dinflammation or autoimmune disorders. The present sequence represents cc the htrb-1 novement ide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  opthalamological; cardiant; cyrostatic; haemostatic; immunosuppressive; antinflammatory; estrogen receptor; fibroblast growth factor; FGF; tumour necrosis factor; TNF; htrb-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel isolated human tribbles homologue-1 polypeptide for inhibiting AP-1-mediated inflammatory signal in a cell, and activating ERK-mediated signal e.g. AP-1-mediated gene activation signal in a constant (A_{\rm c})^2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dower
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            08-JAN-2002; 2002WO-US00070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-OCT-2002
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                                  polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fig 11B; 131pp; English
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The present sequence represents a partial polypeptide which has kinase activity. The kinase polynucleotides can be used to express the polypeptides, and as probes to identify nucleic acids encoding proteins having kinase activity. The kinase polypeptides and fragmented polypeptides are used as molecular weight and isoelectric focusing markers, and as controls for peptide fragmentation. They also have a number of therapeutic uses as kinases play a central role in cellular signal transduction. The polypeptides could also be used to identify binding partner proteins. The polypeptides can also be used as a reagent to identify any proteins that the polypeptide regulates, and proteins with which it might interact. The polypeptides can be used as used for preparation of antibodies. The antibodies can be used in assays to detect the presence of the protein, and to purify the protein by immunoaffinity chromatography.
                                                                                                                                                                                                                                                                                                                                                                                                          04-AUG-1998;
11-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kinase activity; molecular weight marker; isoelectric focusing marker; peptide fragmentation control; cellular signal transduction.
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 Bequence
                                                                                                                                                                                                                                       Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PeptideA JJ503-KS comprising domains VIA to XI of a protein kinase.
                                                                                                                                                                                                                                                                 weight
                                                                                                                                                                                                                                                                                 New human
                                                                                                                                                                                                                                                                                                                                                    Virca
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  360
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98US-0099972
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Query Match

. 61

Score

1675;

В 21;

Length

360

The invention provides PKIN. The PKIN polypept

polypeptides

human kinases (PKIN) a

and polynucleotides encoding using standard recombinant

Claim 1; Page 115; 126pp; English.

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Best Local Similarity 99. 
Matches 317; Conservative
                                                                                                                                       Tang YT, Bu
Hafalia A,
Zingler KA,
                                                                                                                                                                                                                   17-FEB-2000;
02-MAR-2000;
09-MAR-2000;
17-MAR-2000;
                                                    isolated human kinase polypeptides useful in the diagnosis, treatm and prevention of cancer, immune disorders and disorders affecting growth and development -
                                                                                               WPI; 2001-514771/56.
N-PSDB; AAH76218.
                                                                                                                                                                                                                                                                                                  23-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                PKIN; kinase; cytostatic; immunosuppressive; immunostimulant; human; antiarteriosclerotic; cardiant; gene therapy; antisense therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                       29-OCT-2001
                                                                                                                               Nguyen DB,
                                                                                                                                                                                                                                                                           16-FEB-2001;
                                                                                                                                                                                                                                                                                                                      WO200160991-A2
                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                  Human kinase
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                                                                                                                             Buford N, Gandhi AR,
, Shih LL, Tribouley
A, Lu DAM, Bandman O,
, Lal P, Walsh RT;
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; 2000US-0186559.
; 2000US-0188606.
; 2000US-0189998.
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l; Mismatches
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y CM, Yao MG,
O, Policky JL,
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Burrill JD,
Griffin JA,
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Thornton
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Best Local &
Matches 308
                                                                                                                                                                                                                      diagnosis; cytostatic; proliferative; vulnerary; immunomodulator; antidiabetic; antiasthmatic; antirheumatic; antiarthritic; antiviral; antiinflammatory; antiproid; antiarthritic; antiarthritic; antiarthritic; antiarthritic; antiarthritic; coagulant; nootropic; dermatological; neuroprotective; thrombolytic; coagulant; nootropic; vasotropic; antiporiatic; antiangiogenic; gene therapy; inflammation; immune disorder; haematopoietic cell disorder; autoimmune disorder; allergic reaction; graft versus host disease; organ rejection; haematopoietic; thrombolytic; cardiovascular disorder; infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          methodology. The PKIN polypeptides, polynucleotides, modulators and specific antibodies are useful in the diagnosis, treatment and prevention of cancer, immune disorders, disorders affecting growth and development, atherosclerosis, and sorder cardiovascuar diseases, and lipid disorders and in the assessment of the effects of exogenous compounds on the expression of nucleic acid sequences of human kinases. The present sequence represents a human PKIN-10 polypeptide.
                                                                                                                                                                                                                                                                                                                                              Human; cancer associated gene; cancer
                                                                                       08-MAR-2000;
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                               (HUMA-) HUMAN GENOME
                                                                                                                                                                                  eapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AADVWSLGVALFTMLAGHYPFQDSEPVLLFGKIRRGAYALFAGLSAFARCLVRCLLRREF 300
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                                                                                         2000WO-US05882.
                                                                                                                                                                                                                disease;
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                                 SCI INC
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Pred. No. 2e-1:
4; Mismatches
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CC include: cytostatic; proliferative; vulnerary; immunomodulator; CC antidiabetic; antiasthmatic; antirheumatic; antiarthritic; antivitasthmatic; antialthritic; antialitadiabetic; antiasthmatic; antialthritic; CC antiinflammatory; antithyroid; antiallergic; antibacterial; antivital; CC antiinflammatory; antithyroid; cardiant; thrombolytic; coagulant; CC dermatological; neuroprotective; cardiant; thrombolytic; coagulant; CC nootropic; vasotropic; antipsoriatic and antianglogenic. The CC polynucleotides and polypeptides can be used for preventing, treating or CC northing medical conditions and diagnosing pathological conditions. CC polynucleotides, polypeptides, antibodies, sonists and antagonists from CC immune colls; the proliferation, differentiation or mobilisation of CC immune colls, to treat disorders of haematopoletic cells, autoimmune CC disorders, modulate haemostatic or thrombolytic activity, modulate rejection, cancers, cardiovascular disorders, neurological disease and CC bacterial or viral infections. The peptides, nucleotides, antibodies, agonists and antagonists may be also be used in drug screens. AAC/8449 to AAR/8459 and AAR/84240 represent sequences used in the exemplification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              in AAB43398 to AAB44239. The proteins can have activities based on it tissues and cells the genes are expressed in. Example of activities include: cytostatic; proliferative; uninexact.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel isolated nucleic useful for treating or
Sequence
                                                                                   present invention
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)B; AAC77866.
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233
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S 밁 ঠ 밁 S S Query Match Best Local S Matches 208 206 331 146 271 211 GPDDSLWDKHACPAYVGPBILSSRASYSGKAADVWSLGVALFTMLAGHYPFQDSBPVLLF 151 RHRIPBPEAAVLFRQMATALAHCHQHGLVLRDLKLCRFVFADRBRKKLVLENLEDSCVLT 98 26 Similarity GKIRRGAYALPAGLSAPARCLVRCLLRREPAERLTATGILLHPWLRQDPMPLAPTRSHLW BAAQVVPDGLGLDBARBBBGDRBVVLYG EAAQVVPDGLGLDBAREEEGDREVVLYG GPDDSLWDKHACPAYVGPBILSSRASYSGKAADVWSLGVALFTMLAGHYPFQDSBPVLLF RHRIPEPEAAVLFRQMATALAHCHQHGLVLRDLKLCRFVFADRERKKLVLENLEDSCVLT GKIRRGAYALPAGLSAPARCLVRCLLRREPABRLTATGILLHPWLRQDPMPLAPTRSHLW Conservative 58.3%; Score 1102; DB 21; 100.0%; Pred. No. 9.2e-97; Live 0; Mismatches 0; 233 Indels Length 0 Gaps 330 145 270 85

0

ABB06093 standard; Protein; 278

Human NS protein sequence SEQ ID NO:185.

10-MAY-2002

(first entry)

ARBOULT 9
ARBOGO 3
ID ARBO
XX ARBO
XX ARBO
XX ARBO
XX Huma
XX Huma
XX Huma
XX Huma
XX Huma
XX ARO
XX Human; cytostatic; osteopathic; gynaecological; neuroprotective; antirheumatic; antiarthritic; antipsoriatic; ophthalmological; anti-HIV; vasotropic; antiarteriosclerotic; antiinflammatory; dermatological; anorectic; muscular; antiinfertility; cardiovascular; anticosgulant; antifibrinolytic; hypotension; antiasthmatic; immunomodulator; cardiant; anticonvulsant; antidiabetic; tranquilliser; antidepressant; aeuroleptic; gastrointetinal; virucide; antiulcer; cerebroprotective; nootropic; contraceptive; vaccine; gene therapy; cancer; osteoporosis; dystonia; endometriosis; degenerative disease; multiple sclerosis; psoriasis;

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CC encoding the proteins given in ABB06037 to ABB06164. The novel sequences (NS) can have cytostatic, osteopathic, synascological, neuroprotective, antirheumatic, antiarthritic, antiporiatic, ophthalmological, virucide, care vasotropic, antiarterioselerotic, antiinflammatory, dermatological, cardiant, antifibrinolytic, antiinflammatory, dermatological, cardiant, cardiovascular, antifibrinolytic, antidiabetic, cardiovascular, cardiovascular, cardiovascular, antidiabetic, cardiovascular, cardiovascular, antidiabetic, cardiovascular, cardiovascular, antidepressant, gastrointestinal, aeuroleptic, cerebroprotective, antidepressant, gastrointestinal, aeuroleptic, cerebroprotective, cardiovascular, antidepressant, gastrointestinal, aeuroleptic, cerebroprotective, contropic and contraceptive activities. The NS can be used in vaccines, cerebroprotective, antibodiss from the present invention can be used for treating and contropic and antisonascular cardiovascular, steroposis, multiple sclerosis, redometriosis, degenerative disease, dystonia, multiple sclerosis, rheumatoid arthritis, psoriasis, cataracts, restenosis, atherosclerosis, inflammation, skin disorders, cataracts, restenosis, atherosclerosis, inflammation, skin disorders, cataracts, restenosis, atherosclerosis, infertility, cardiovascular contesses, epilepsy, angina, neurodegeneration, disbetes, anxiety, anticut, antidisease, infertility, cardiovascular, contessed, schemia, viral disease, gastric ulcers, stroke, altheimar's disease and as contraceptive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 209; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       rheumatoid arthritis; cataract; restenosis; atherosclerosis; glaucoma; inflammation; skin disorder; obesity; muscular dystrophy; AIDS; infertility; cardiovascular disease; coagulation disease; hypertension; ischaemia; asthma; immune disease; epilepsy; angina; neurodegeneration; disbetes; anxiety; depression; schizophrenia; viral disease; stroke; gastric ulcer; Alzheimer's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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15-DEC-2000; 2000IL-0140354.
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                                                                                                                                    ARPTEVLAGTOLLYAFFTRTHGDMHSLVRSRHRIPEPEAAVLFRQMATALAHCHQHGLVL
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                                                                                              ARPTEVLAGTQLLYAFFTRTHGDMHSLVRSPHRIPEPEAAVLFRQMATALAHCHQHGLVL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            278 AA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 58.0%;
99.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bernstein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 1097; DB 23; Length Pred. No. 3.5e-96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                      211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       278;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0,
                                                                                                                                                               180
                                                                                                                                                                                                                                                                                                       120
                                                                                                                                                                                                                                   148
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Human NS protein sequence SEQ ID NO:200
                                                                                                           ABB06108;
                                                                                                              ABB06108 standard; Protein; 278
                                                                                                 cytostatic; osteopathic;
                                                                                                       (first entry)
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antirheumatic; antiarthritic; antipsoriatic; ophthalmological; anti-HIV; vasotropic; antiarteriosclerotic; antiinflammatory; dermatological; anorectic; muscular; antiinfertility; cardiovascular; anticoagulant; antifibrinolytic; hypotension; antiasthmatic; immunomodulator; cardiant; anticonvulsant; antidabetic; tranquilliser; antidepressant; aeuroleptic; gastrointestinal; virucide; antilicer; cerebroprotective; nootropic; contraceptive; vaccine; gene therapy; cancer; osteoporosis; dystonia; endometriosis; degenezative disease; multiple sclerosis; dystonia; endometriosis; degenezative disease; multiple sclerosis; glaucoma; inflammation; skin disorder; osteopity; muscular dystrophy; AIDS; infertility; cardiovascular disease; cosgulation disease; hypertension; ischaemia; asthma; immune disease; cosgulation disease; stroke; anticox; depression; schizophrenia; viral disease; stroke; ulcer; Alzheimer's disease. gymaecological; neuroprotective;

Homo

WO200206315-A2

24-JAN-2002.

17-JUL-2001; 2001WO-IL00653

18-JUL-2000; 2000IL-0137345. 15-DEC-2000; 2000IL-0140354.

(COMP-) COMPUGEN LTD

Mintz L, Freilich S,

One hundred and twenty eight novel nucleic acid sequences, useful for treating and diagnosing e.g. cancer, asthma and Alzheimer's -

Claim 6; Page 231-232; 290pp; English.

CC encoding the proteins given in ABB06037 to ABB06164. The novel sequences (CNS) can have cytostatic, osteopathic, synascological, neuroprotective, cantirheumatic, antiarthritic, antipsoriatic, ophthalmological, virucide, CC antirheumatic, antiarteriosclerotic, antiinfelmmatory, dermatological, CC anorectic, muscular, anti-HIV, antiinfertility, cardiovascular, CC anticosgulant, antifibrinolytic, hypotension, antiasthmatic, cardiant, CC immunomodulator, anticonvulsant, antidiabetic, tranquilliser, antiulcer, CC antidepressant, gastrointestinal, aeuroleptic, cerebroprotective, CC noctropic and contraceptive activities. The NS can be used in vaccines, CC gene therapy and antisense therapy. Nucleic acids, expression vectors and CC diseases, go, cancer, osteoporosis, endometriosis, degenerative CC diseases, dystonia, multiple sclerosis, rheumatoid arthritis, psoriasis, CC cataracts, restenosis, atherosclerosis, inflammation, skin disorders, CC glaucoma, obesity, muscular dystrophy, AIDS, infertility, cardiovascular CC disease, coagulation disease, inclammation, skin disorders, CC disease, schippsy, angina, neurodegeneration, disbetee, anxiety, CC depression, schizophrenia, viral disease, gastric ulcers, stroke, CV Alzheimer's disease and as contraceptive. ABL39691 to ABL39818 represent novel human nucleic acid sequences encoding the proteins given in ABB06037 to ABB06164. The novel sequences and

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ABBOULT 11
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Best Local
The invention provides an isolated human tribbles homologue-1 (htrb-1, also known as stress kinase inhibitor protein (SKIP-1)) polypeptide. The htrb polypeptide is useful for inhibiting an AP-1 mediated inflammatory signal in a cell. The polypeptide employed in the method is preferably htrb-3 N c. It is also useful for providing htrb agonist activity for activating an ERK-mediated signal e.g. AP-1-mediated gene activation signal, an estrogen receptor-mediated gene activation signal, an estrogen receptor-mediated gene activation signal, an a cell. Htrb modulators are useful for modulating AP-1 mediated inflammatory signal in a cell such as tumor necrosis factor (TMP) induced inflammatory signal in a cell such as tumor necrosis factor (TMP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; tribbles; htrb-1; stress kinase inhibitor protein; SKIP-1; AP-1; antirhoumatic; antiarthritic; antidiabetic; antipsoriatic; osteopathic; opthalamological; cardiant; cytostatic; haemostatic; immunosuppressive; antinfilammatory; estrogen receptor; fibroblast growth factor; FGF; tumour necrosis factor; TNF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel isolated human tribbles homologue-1 polypeptide for inhibiting AP-1-mediated inflammatory signal in a cell, and activating ERK-mediated signal e.g. AP-1-mediated gene activation signal in a cell
                                                                                                                                                                                                                                                                                                                                                                                              Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08-JAN-2001; 2001US-260294P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          08-JAN-2002, 2002WO-US00070.
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DB; ABN86478.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RDLKLCRFVFADRERKKLVLENLEDSCVLTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AVATASRLGPYVLLEPEEGGRAYRALHCPTGTEYTCKYYPVQEALAVLEPYARLPPHKHV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RDLKLCRFVFADRERKKLVLENLEDSCVLTG
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                                                                                                                                                                                                                                                                                                                                                                                       10B; 131pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             homologue-1 (htrb-1)
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Pred. No. 3.5e
1; Mismatches
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Best Local Simi
Matches 162;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  signal. htrb proteins are useful in screening assays, predictive medicine and in therapeutics or prophylactics. The htrb proteins are useful for screening compounds e.g. for treating and/or preventing diseases caused by abnormal htrb activity, such as rheumatoid arthritis, diabetes, psorissis, osteoporosis, diabetic retinopathy, myocardial infarction and cancers. The htrb therapeutics are useful for antagonizing interleukin-1 dependent disorders of human placenta, intraventricular hemorrhage, neonatal white matter damage and subsequent cerebral palsy; and inflammation or autoimmune disorders. The present sequence represents the htrb-1 polypeptide.
AAU28135 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                     316
                                                                                                                        293
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                                                                                                                                                                              RSLLRREPSERLTAPEILLHPWFESVLEP-GYIDSEIGTSDQIVPE
                                                                                                                      RCLLRREPAERLTATGILLHPWLRQDPMPLAPTRSHLWEAAQVVPD
                                                                                                                                                       TTGTYSGKAADVWSLGVMLYTLLVGRYPFHDSDPSALFSKIRRGQFCIPEHISPKARCLI
                                                                                                                                                                                                                              CHQSAIVLGDLKLRKFVFSTBERTQLRLESLEDTHIMKGEDDALSDKHGCPAYVSPBILN
                                                                                                                                                                                                                                                  CHQHGLVLRDLKLCRFVFADRERKKLVLENLEDSCVLTGPDDSLWDKHACPAYVGPBILS
                                                                                                                                                                                                                                                                                                  QLPSHSNITGIVEVILGETKAYVFFEKSFGDMHSYVRSRKRLREEBAARLFKQIVSAVAH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RATPLAAPA-GSLSRKKRLELDD--NLDTERPVQKRARSGP---QPRLPPCLLPLSPPTA
                                                                                                                                                                                                                                                                                                                                                                         PGAGGGSGSAPGPSRIADYLLLPLABREHVSRALCIHTGRELRCKVFPIKHYQDKIRPYI
                                                                                                                                                                                                                                                                                                                                                                                                        PDRATAVATA---SRLGPYVLLEPEEGGRAYRALHCPTGTEYTCKVYPVQBALAVLEPYA 112
                                                                                                                                                                                                                                                                                                                                                                                                                                             RGPALLFPATRGVPAKRLLDADDAAAVAAKCPRLSBCSSPPDYLSPPGSPC-SPQPPPAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        372 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                39.4%; Score 744.5; DB 2
46.8%; Pred. No. 2.3e-62;
tive 47; Mismatches 126
269
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   126;
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                                                                                     360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       372,
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ARESULT 12
AAU28135
ID AAU2833
XX AAU28
AC AAU28
AC AAU28
XX Novel
DE Novel
XX Humar
KW Humar
KW Lrant
KW Lrant
KW Ulcel
KW Ulcel
KW Gut I
KW Homo
XX Homo
                                                                                                                                                                                                                                                                                                                              transgenic animal; Alzheimer's disease; Parkinson's disease; burn; amyotrophic lateral sclerosis; platelet disorder; thrombocytopenia; ulcer; osteoporosis; bone degenerative disorder; periodontal disease; gut protection; lung; liver fibrosis; immune deficiency; infection; severe combined immunodeficiency; SCID; autoimmune disorder; allergy; multiple sclerosis; rheumatoid arthritis; diabetes mellitus; asthma; multiple sclerosis; rheumatoid arthritis; diabetes mellitus; asthma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ischaemia-reperfusion injury; haematopoiesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; secreted protein; arthritis; Crohn's disease; sepsis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel human
                                                                                                                                                                                                                                                                                                           fertility;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAU28135
                                                                                                                                                                                                                                                                                                           analgesic; pain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     secretory protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry
                                                                                                                                                                                                                                                                                                           antigen.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cancer; neuropathy;
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shock;

07-MAR-2000; 19-MAY-2000; 17-JUN-2000;

2000US-0519705. 2000US-0574454. 2000US-0596193.

05-MAR-2001,

2001WO-US04942

13-8BP-2001

Homo

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cc and polynucleotides (II) (II) and (II) are useful for treating inflammatory conditions such as arthitis, nephitis, Crohn's disease, cc inchaemia reperfusion injury, shock, sepsis, immune responses, and is ci sichaemia reperfusion injury, shock, sepsis, immune responses, and is cc involved in increasing haematopolesis, stem cell survival, bone growth cc and remodeling, (I), (II) and modulators of (II) are useful for creating transgenic animals useful for studying the in vivo activities of (C prophylaxis or treatment of one or more cancers. (II) is also useful for the polypeptide as well as for studying modulators of the polypeptides. (I) induces the proliferation of neural cells and regeneration of nerve cc and brain tissue and is useful for the treatment of central and cc parigheral nervous system diseases and neuropathies, such as Alzheimer's, cr parkinson's diseases and neuropathies, such as Alzheimer's, cativity, regulation of haematopoises and is useful for treating myeloid cc activity, regulation of haematopoises and is useful for treating myeloid cc and for regeneration of bone, cartilage, tendon, ligament and/or nerve tissue growth, and in tissue repair, healing of burns, incisions, cu lears, for treating osteoporosis, osceoarthritis, bone degenerative disorders, for treating severe combined immune deficiencies and cc disorders including severe combined immune deficiency (SCID), bacterial or fungal infections, autoimmune disorders e.g. multiple sclerosis, respectively and can act as an antigen in a vaccine composition to raise an colar sequences of the tinyantion.
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Best Local S
Matches 133
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19-SEP-2000;
20-OCT-2000;
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Zhao
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HDSDPSALPSKIRRGOFCIPEHISPKARCLIRSLLRREPSERLTAPBILLHPWFESVLEP
                                   QDSSPVLLFGKIRRGAYALPAGLSAPARCLVRCLLRREPABRLTATGILLHPWLRQDPMP
                                                                                                                                              NLEDSCYLTGPDDSLWDKHACPAYVGPEILSSRASYSGKAADVWSLGVALFTMLAGHYPP
                                                                                                                                                                                          GDMHSYVRSRKRLREEBAARLFKQIVSAVAHCHQSAIVLGDLKLRKFVFSTEERTQLRLE
                                                                                                                                                                                                                                                                                           CPGRCASTLGRRVRCKVFPIKHYQDKIRPYIQLPSHSNITGIVEVILGETKAYVPFEKDF
                                                                                                                                                                                                                                                                                                                                         CP----TGTEYTCKVYPVQEALAVLEPYARLPPHKHVARPTEVLAGTQLLYAFFTRTH
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Yang
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2000US-0665363.
2000US-0693267.
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Pred. No. 1.
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                                                                                                                                                                                                                                                                                                                                                                                                           .5e-56;
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Wang.
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19-MAY-2000;
17-JUN-2000;
14-JUL-2000;
19-SEP-2000;
20-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ischaemia-reperfusion injury; haematopoiesis; cancer; neuropathy; transgenic animal; Alzheimer's disease; Parkinson's disease; burn; amyotrophic lateral sclerosis; platelet disorder; thrombocytopenia; ulcer; osteoporosis; bone degenerative disorder; periodontal disease; gut protection; lung; liver fibrosis; immune deficiency; infection; severe combined immunodeficiency; SCID; autoimmune disorder; allergy; multiple sclerosis; rheumatoid arthritis; diabetes mellitus; asthma;
                                                                                                                                                                                                                                                                                                                                                                        05-MAR-2001; 2001WO-US04942
                                                                                                                                                                                                                                                                                                                                                                                                              WO200166689-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; secreted protein; arthritis; Crohn's disease; sepsis; shock;
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                                                                                                                                                                                                                                                                                        (HYSE-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                fertility; analgesic; pain; antigen.
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; 2000US-0574454.
; 2000US-0596193.
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Novel polypeptides and nucleic acids obtained from cDNA libraries prepared from various human tissues, for diagnosis and treatment cancer, neurological, inflammatory, and autoimmune disorders -얁

Tang Zhao

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Liu C

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Asundi V, Drmanac

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C, We Zhang

Wehrman T, ang J, Chen

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Y, Wang zhou ng J;

WPI; 2001-589934/66.

Example 2 SEQ ID No 680; 107pp; English.

The invention relates to novel isolated human secreted polypeptides (I) CC and polynucleotides (II). (I) and (II) are useful for treating CC inflammatory conditions such as arthritis, nephritis, Crohn's disease, CC ischaemia-reperfusion injury, shock, sepsie, immune responses, and is CC involved in increasing haematopolesis, stem cell survival, bone growth CC and remodeling. (I), (II) and modulators of (II) are useful for CC prophylaxis or treatment of one or more cancers. (II) is also useful for CC creating transgenic animals useful for studying the in vivo activities of the polypeptide as well as for studying modulators of the polypeptides. (I) induces the proliferation of neural cells and regeneration of nerve and brain tissue and is useful for the treatment of central and cCC entipheral nervous system diseases and neuropathies, such as Alzheimer's, CC Parkinson's disease, Huntington's disease, and amyotrophic lateral CC excivity, regulation of haematopoiesis and is useful for treating myeloid or sclerosis. In addition, (I) is involved in chemotactic or chemokinetic corruphoid cell disearchers, platelet disorders such as thrombocytopenia and for regeneration of bone, cartilage, tendon, ligament and/or nerve tissue growth, and in tissue repair, healing of burns, incisions,

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Best Local S
Matches 127
WPI, 2003-278653/27.
N-PSDB; ACC45125, AC
                                                                                                                                                                                                                  27-AUG-2001;
31-OCT-2001;
                                                                                                                                                                                                                                                                                                          27-AUG-2002; 2002WO-US27187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human, phosphoprotein regulating mitogenic pathway gene, cytostatic, vaccine, cancer, C8FW.
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127; Conserv
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2001US-330797P
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51.2%; Pred. No. 2.1e-54;
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Claim 16; Page 86; 86pp; English.
                                                                                                                                                         cancers
                                                                                                                                                               Diagnosing, preventing, treating and prognosticating a cancer in a mammal by detecting and measuring the CBFW gene copy number and/or CB level, useful for breast, brain, lung, colon, ovarian and/or prostate
                                                                                                                                                                            CBFW
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The present invention describes a method for diagnosing a cancer in a mammal. The method comprises detecting and measuring the C8FW gene copy number or level in a biological subject from a region of the mammal that is suspected to be pre-cancerous or cancerous to generate data for a test gene copy, and comparing the test gene copy number or level to a data for a control gene copy number or level, where an amplification of the gene in the biological subject relative to the control indicates the presence of a pre-cancerous lesion or cancer in the animal. C8FW has cytostatic activity, and can be used in vaccines. The method can be used for the diagnosis, prevention, treatment and prognostication of breast, colon, lung, brain, prostate and/or ovarian cancer. The present sequence represents human C8FW from the present invention. C8FW is a phosphoprotein regulating mitogenic pathway protein.

Sequence 206 AA;

DB 24;

Length

206;

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Best Local Similarity 57.9
Matches 113; Conservative
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                                                                                                                                                                   144 MHSLVRSRHRIPEPENAVLFRQMATALAHCHQHGLVLRDLKLCRFVFADRERKKLVLENL
180
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YIDSEIGTSDQIVPE 194
                        PTRSHLWEAAQVVPD 338
                                                  SDPSALFSKIRRGQFCIPEHISPKARCLIRSLLRREPSERLTAPEILLHPWFESVLEP-G 179
                                                                  SEPVLLFGKIRRGAYALPAGLSAPARCLVRCLLRREPAERLTATGILLHPWLRQDPMPLA
                                                                                                    EDTHIMKGEDDALSDKHGCPAYVSPEILNTTGTYSGKAADVWSLGVMLYTLLVGRYPPHD
                                                                                                                   BDSCVLTGPDDSLWDKHACPAYVGPEILSSRASYSGKAADVWSLGVALFTMLAGHYPFQD
                                                                                                                                                       MHSYVRSRKRIREEEAARIFKQIVSAVAHCHQSAIVLGDIKLRKFVFSTEERTQIRLESI
                                                                                                                                                                                                                     30.6%;
                                                                                                                                                                                                      29;
                                                                                                                                                                                                        Score 578.5; I
Pred. No. 7.1e.
29; Mismatches
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RESULT 15 ABB71379 ID ABB71 XX ABB71 XX ABB71 XX Drosc XX

ABB71379 standard; Protein; 484

ABB71379;

26-MAR-2002 (first entry)

Drosophila melanogaster polypeptide SEQ ID NO 40929

Drosophila, developmental biology; cell signalling; insecticide; pharmaceutical.

Drosophila melanogaster.

WO200171042-A2

27-SEP-2001.

23-MAR-2001; 2001WO-US09231

23-MAR-2000; 11-JUL-2000; 2000US-191637P. 2000US-0614150.

(PEKE) PE CORP NY.

Venter JC, Adams Z, Į. DWD, Myers EE

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Best Local S
Matches 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invent: useful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLIG1617-ABLIG171), expressed DNA sequences (ABLIG187-ABLIG175) and the encoded proteins (ABB7737-ABB72072).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-656860/75.
N-PSDB; ABL15482.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; SEQ ID NO 40929; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
326
                                                                                                              244 VWSLGVALFTMLAGHYPFQDSBPVLLFGKIRRGAYALPAGLSAPARCLVRCLLRREPAER 303
                                                                                                                                                                              184 KLCRFVFADRERKKLVLENLEDSCVLTGPDDSLMDKHACPAYVGPEILSSRASYSGKAAD 243
                                                                                                                                                                                                                                                                      134 YA------PFTRTHGDMHSLVRGRHRIPEPEAAVLFRQMATALAHCHQHGLVLRDL 183
                                                                                                                                                                                                                                                                                                                      148
                                                                                                                                                            266
                                                                                                                                                                                                                                      206 IAPVPQERDSTGGVTGVYENLHTYIRHAKRLCETEARAIFHQICQTVQVCHRNGIILRDL 265
                                                                                                                                                                                                                                                                                                                                                                                                104 IQQRYLISAQPSHISAAVAAKTP-ASYRHLVDLTASNL-------RCVDIFT 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tch 23.0%; Score 435; DB 22; Length 484; al Similarity 33.4%; Pred. No. 1.1e-32; 116; Conservative 45; Mismatches 134; Indels 52;
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                                                                                                                                                                                                                                                                                                                                                           91
                                                                                                                                                          KLKRFYPIDEARTKLQYESLEGSMILDGEDDTLSDKIGCPLYTAPELLCPQQTYKGKPAD 325
                                                                                                                                                                                                                                                                                                                  GEOFLCRI -- VNEPLHKVORAYFOLOQHDEELRRSTIYGHPLIRPVHDIIPLTKDRTYIL 205
                                                                                                                                                                                                                                                                                                                                                         GTEYTCKVYPVQEAL-AVLEPYARLPPHKHVARPTEVLA-------GTQLL 133
                                                                                                                                                                                                                                                                                                                                                                                                                                VOKRARSGPOPRIPPCILPISPPTAPDRATAVATASRIGPYVILBPEBGGRAYRALHCPT 90
                                                                            MWSLGVILYTMLVGQYPFYEKANCNLITVIRHGNVQIPLTLSKSVRWLLLSLLRKDYTER 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          484 AA;
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Search completed: January 15, 2004, 14:57:50 Job time : 46 secs

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Result
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Maximum DB
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Perfect score:
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11
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seq length: 2000000000
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                                                                                                                                                                                                   Match
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358
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SPTREMBL 23:*
   GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.
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sp_bacteria:*
sp_fungi:*
sp_human:*
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sp_virus:*
sp_vertebrate:*
sp_unclassified:*
sp_rvirus:*
sp_bacteriap:*
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sp_phage:*
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                        3443
37443
3772
3772
3172
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1 Q8K017
015180
0 Q9EQL6
Q96RU8
Q96RU8
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Q92519
Q28283
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Q91W04
Q8H7S4
Q9F3C2
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         Q8r2v8 mus musculu
Q92519 homo sapien
Q28283 canis famil
Q8k4k3 mus musculu
Q15180 homo sapien
Q9eq16 rattus norv
Q96ru8 homo sapien
Q9h2y8 homo sapien
Q9h2y8 homo sapien
Q9h2y8 mus musculu
Q91w04 mus musculu
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Q91g2c streptomyce
Q18041 caenorhabdi
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arabidopsis
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Q8QWS9	048660	Q8K4U2	QBU8M5	Q9Z4Y0	Q8GY77	Q9IH80	Q9WVS3	Q9VVC9	Q9GMD3	Q8FY69	6MLX80	Q9HZG0	QBIVPS	041253	Q8TBX5	Q9H6R5	Q8C0V7	Q9RDL4	Q8SD32	Q9BYG4	Q8F930	Q9AQV3	Q8BNY7	Q9JJD6	Q9NS63	Q9L184	Q9EZ07	Q92XU5
Q8qw89 norwalk vir	etaphylo		agro	-	Q8gy77 arabidopsis	Q9ih80 cherry necr	Q9wvs3 mus musculu		Q9gmd3 bos taurus	Q8fy69 brucella su		Q9hzg0 pseudomonas	homo e	O41253 rice ragged		homo	91m	Q9rdl4 streptomyce	Q8sd32 pseudomonas	3	_		Q8bny7 mus musculu	Q9jjd6 mua muaculu	5	Q91184 streptomyce	Q9ez07 streptomyce	Q92xu5 rhizobium m

ALIGNMENTS

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RESULT 1

QRR2VB

ID QBR2VB

AC QBR2

DT 01-3

DT 01-3

DT 01-4

DT 01-4

CO Man

OC Buk

OC Buk

OC Buk

CO Man

OC NCB

RN [1]

RP SE(

RA St;

RL Sul

DR EM

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DR PF

NW PF

NW SQ S;
RESULT 2
Q92519
ID Q925
AC Q925
DT 01-F
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                                                                                                                        Query Match
Best Local S
Matches 14
Q92519 |
Q92519;
01-FEB-1997
                                                                                                                                                               01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical 29.2 kDa protein (Fragment).
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                               Q8R2V8
                                                                                                                                                                                                                                                                                                                      Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                   EQUENCE FROM N.A.
                                                                                           236 SYSGKAADVWSLGV 249
                                                                             143
                                                                                                                       14; Conservative 0;
                                                                            SYSGKAADVWSLGV 156
(TrEMBLrel. 02, Created)
                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                      3.9%; Score 14; DB 11; Length 257; 100.0%; Pred. No. 5.1e-05; Indels
                     PRT;
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Best Local S
Matches 14
                                                                                                                        TISSUB=Thyroid;
MEDLINE=98000262; PubMed=9342215;
Wilkin F., Suarez-Huerta N., Robaye B., Peeter Dumont J.B., Maenhaut C.;
Pumont J.B., Maenhaut C.;
"Characterization of a phosphoprotein whose mR mitogenic pathways in dog thyroid cells.";
Eur. J. Biochem. 248:660-669(1997).
EMBL; X99144; CAA67581.1; -.
HSSP; Q63450; 1A06.
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01-MAR-2003 (Tr)
GS3955 (GS3955)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1996
01-NOV-1996
01-MAR-2003
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Submitted (FEB-2001) to the EMBL/
EMBL; D87119; BAA13250.1; -.
EMBL; BC002637; AAH02637.1; -.
HSSP; Q63450; 1A06.
InterPro; IPRO00719; Prot_kinase.
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Q28283;
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TISSUE=Cancellous bone;
Ohno I., Hashimoto J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Identification and Characterization of N
Thyroid of Dogs Treated with Methimazole
J. Biol. Chem. 271:28451-28457(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PP00069; pkinase; 1.
ProDom; PD000001; Prot kinase; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
ATP-binding; Transferase.
SEQUENCE 343 AA; 38800 MW; BF8B7366D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ohno I., Hashimoto J., Takac
Submitted (AUG-1996) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
Pfam, PF00069; pkinase; 1.
ProDom; PD000001; Prot kinase; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Canis familiaris (Dog).
Eukaryota; Metazoa; Chordata; (
Mammalia; Eutheria; Carnivora;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CSFW ORF protein CSFW ORF.
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MBDLINE=97067069; PubMed=8910471;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9615;
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                                                                                        InterPro, IPR000719; Prot_kinase.
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EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Craniata; Vertebrata;
; Fissipedia; Canidae;
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Matches 14
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Best Local S
Matches 14
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InterPro; IPR001295; Ser thr_pkinase.
InterPro; IPR001245; Tyr_pkinase.
Pfam; PP00069; pkinase; 2.
ProDom; PD000001; Prot_kinase; 1.
SWART; SM00220; S_TKC; 1.
SWART; SM00219; TYrKC; 1.
PROSITE; PS50011; PROTEIN KINASE_DOM; 1
ATP-binding; Transferase.
SEQUENCE 343 AA; 38758 MW; 0B3965881
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Q8K4K3;
01-OCT-2002
01-OCT-2002
01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                        Q8K017
Q8K017;
01-OCT-2002
                                                                            TISSUB-Kidney;
Strausberg R.;
Submitted (JUL-2002)
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SEQUENCE 343 AA; 38786 MW;
  SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Aorta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         activated protein kinase signaling.";
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AF358867; AAM45477.1; -..
                                                                                                                                                                                                              NCBI_TaxID=10090;
                                                                                                                                                                                                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                             TRB-2 (CSFW ORF prot
Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus
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lnase signaling.";
                                                                                                                                                                                                                                                Rodentia;
                                                                                                                                                                                                                                                                   Chordata;
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Pred. No.
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Sciurognathi; Muridae;
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  and
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6.7e-05;
hes 0;
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Cerebellum,
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L.A.J., Qwa
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                                                                                                                                                                                                                                                                      Euteleostomi;
  and Retina;
                                                                                                                                                                                                                                                Murinae;
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Matches 13
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"Analysis of the mouse transcriptome based on functional ann
fo,770 full-length cDNAs.";

INATURE 420:563-573(2002).

REMBL; BC034338; AAH34338.1; -.

REMBL; BC034338; AAH34338.1; -.

REMBL; AK040747; BAC32063.1; -.

REMBL; AK080064; BAC37820.1; -.

REMBL; AK080064; BAC37820.1; -.

REMBL; AK080064; BAC38467.1; -.

RINTERPTO; IPR000719; Prot kinase.

RINTERPTO; IPR0002290; Ser Thr pkinase.

RINTERPTO; IPR00145; Tyr pkinase.

RP FABM, PF00069; pkinase; 1.

RP FABM, PF00069; pkinase; 1.

RP FABM, PF00069; STKC; 1.

RR SMART; SM00219; TYRKC; 1.

RR SMART; SM00219; TYRKC; 1.

RR ATP-binding: Transferase.
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  O15180
O15180;
O15180;
O1-JAN-1998 (TEMBLER) 05,
O1-JAN-1998 (TEMBLER) 05,
O1-MAR-2003 (TEMBLER) 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
TISSUB-Thyroid,
MEDLINE-98000262; PubMed-9342215;
Wilkin F., Suarez-Huerta N., Robaye B., Peet
Dumont J.E., Maenhaut C.,
"Characterization of a phosphoprotein whose
                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                    ATP-binding;
                                                                                                                                                                                                                                                        Pfam; PF00069; pkinase; 1.
Probom; PD000001; Prot kinase; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM;
                                                                                                                                                                                                                                                                                                                                     mitogenic pathways in dog thyroid cells.",
Eur. J. Biochem. 248:660-669(1997).
EMBL, AJ000480; CAA04119-1; -.
InterPro, IPRO00719; Prot_kinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bukaryota, Metazoa,
Mammalia, Eutheria,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATP-binding; Transferase.
SEQUENCE 343 AA; 38772 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Thyroid,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=22354683; PubMed=12466851; The PANTOM Consortium,
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112
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                                                                                                                 Similarity
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  YSGKAADVWSLGV
                                         YSGKAADVWSLGV 249
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SYSGKAADVWSLGV 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (JUL-1997)
                                                                                                                                                                                            224 AA;
                                                                                             Conservative 0;
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                                                                                                                                                                                                                                           Transferase.
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Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%;
                                                                                                                                                                                            25479 MW;
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                                                                                             3.6%; Score 13; DB 4; L
100.0%; Pred. No. 0.00043;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3.9%; Score 14; DB 11; 100.0%; Pred. No. 6.7e-05;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL/GenBank/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                          740CD0905F86499B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9418B7AC19FCC23F CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Peetermans J., Libert F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                          mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       databases
                                                                                                                                         Length 224;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 343;
                                                                                                                                                                                                                                                                                                                                                                                                                                             18
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annotation
                                                                                          0;
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                                                                                          Gaps
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                                  Query Match
Best Local S
Matches 13
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Best Local Similarity
Matches 13; Conserv
                                                                      Pfam; PPO0069; pkinase; 1.
ProDom; PD000001; Prot_kinase; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM;
ATP-binding; Transferase.
ATP-binding; Tyansferase.
SEQUENCE 372 AA; 40980 MW; 3E2B5Cf
                                                                                                                                                                                                                                                                                              Q96RU8;
Q96RU8;
01-DEC-2001
01-DEC-2001
01-MAR-2003
                                                                                                                                    Kiss-Toth B., Wylie D.H., Qwarnstrom B.E., Dower S.K.; "Identification of pro-inflammatory cytokine signalling components by transcription expression screening."; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases. EMBL, AP250310; AAK58174.1; -. Interpro, IPR000719; Prot_kinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9EQL6
Q9EQL6;
Q1-MAR-2001 (TrEMBLrel. 16,
01-MAR-2001 (TrEMBLrel. 16,
01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                               Homo sapiens (Human)
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                   SKIP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            G-protein-coupled GIG2.
                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                   NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00069; pkinase; 1.
ProDom; PD000001; Prot kinase; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  receptor-induced gene.";
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases
EMBL; AP205438; AAG35664.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATP-binding; Receptor; Transferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR000719; Prot_kinase.
Pfam; PF00069; pkinase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nitech R.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mayhaue M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=Sprague-Dawley;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'Identification of a novel nuclear factor Gig2,
            237
                                                                                                                                                                                                                                                                                                                                                                                                         253
                                              Similarity
YSGKAADVWSLGV 249
                                                                                                                                                                                                                                                                                                                                                                                                                              YSGKAADVWSLGV 249
                                                                                                                                                                                                                                                                                             (TrEMBLrel. 19, (TrEMBLrel. 19, (TrEMBLrel. 23,
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                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    receptor
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                                             3.6%;
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, Last sequence update)
, Last annotation update)
induced protein GIG2 (Fragment)
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Last annotation updat
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                                            Score 13; DB 4;
Pred. No. 0.00067
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Pred. No.
                                                                                3E2B5C87A4F98FDB CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8F9167FB76DFCD37 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Klaudiny J.,
                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                               372
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thi; Muridae; Murinae; Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 11;
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                                                      Length 372;
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                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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                                                                                                                                                                                       network
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YSGKAADVWSLGV

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RESULT OF STREET OF STREET
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Q8K4K4
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Best Local S
Matches 13
Query Match
Best Local
                                                                                                           activated protein kinase signaling.";
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ dat
EMBL; AP358866; AAM45478.1; -.
InterPro; IPR007019; Prot kinase.
InterPro; IPR002290; Ser thr pkinase.
Pfam; PP00069; pkinase; Z.
ProDom; PD000001; Prot kinase; 1.
SMART; SM00220; S TKc; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
ATP-binding; Transferase.
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01-OCT-2002
01-OCT-2002
01-MAR-2003
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Q9H2Y8,
                                                                                                                                                                                                                                                                                                                                                                                                                                                Kiss-Toth B., Dempsey Bagstaff S.M., Wyllie Dower S.K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       receptor-induced gene.";
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF205437; ARG35663.1; -.
InterPro; IPR000719; Prot_kinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 G-protein-coupled
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01-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q8X4K4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATP-binding; Receptor; Transferase SEQUENCE 372 AA; 41008 MW; 5F54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00069; pkinase; 1.
ProDom; PD000001; Prot_kinase; 1.
PROSITE; PS00011; PROTEIN KINASE DOM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mayhaus M.,
Nitech R.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                    "Mammalian homologe of Drosophila tribbles (htrb) control mitogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ø
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ıl Similarity
13; Conserva
   Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          dney;
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(TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
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HBLrel. 16,
HBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chordata;
Primates;
                                                                                           41282 MW;
3.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C., Jo
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i., Harte M.,
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induced protein GIG2.
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Score 13;
Pred. No.
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Craniata; Vertebrata; Butelo Catarrhini; Hominidae; Homo
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                                                                                           3A3DE82B46CD907F CRC64;
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      NO.
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   DB 11;
0.00067;
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RESULT 12
Q8H7S4
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AC Q8H7S
AC Q8H7S
AC 0H7S
DT 01-MA
DT 01
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ID Q91W1
Q91W1
ID Q91W2
ID Q91W2
ID Q91W2
ID O1-DE
DT O1-DE
DT O1-DE
DT O1-MA
DT SINII
OS Mus m
CC Mamma
OX NCEL
RN [1]
RN [2]
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EMBL; AK028626; BAC26038.1; -.
InterPro, IPR00719; Prot_kinase.
Pfam; PF00069; pkinase; 1.
ProDom; PD000001; Prot_kinase; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
ATP-binding; Transferase.
SEQUENCE 372 AA; 41281 MM; AD29BB4E640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q91W04 PRELIMINARY; PRT; 3
Q91W04;
Q91W04;
O1-DEC-2001 (TrEMBLrel. 19, Created)
O1-DEC-2001 (TrEMBLrel. 19, Last seque
O1-MAR-2003 (TrEMBLrel. 23, Last annot
Similar to phosphoprotein regulated by
Mus musculus (Mouse).
                        SEQUENCE FROM N.A.

Wing R.A., Yu Y., Soderlund C
Currie J., Collura K.;

"Rice Genomic Sequence.";

Submitted (OCT-2002) to the B
EMBL; AC107226; AANS2742.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q8H7S4;
Q8H7S4;
01-MAR-2003
01-MAR-2003
01-MAR-2003
                                                                                                                                                                                                                                                    NCBI_TaxID=39947,
                                                                                                                                                                                                                                                                                          Oryza sativa (japonica cultivar-group).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                             Hypothetical protein. OSJNBA0081P02.7.
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Nature 420:563-573(2002).
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STRAIN=C57BL/6J; TISSUE=Skin;
MEDLINE=22354683; PubMed=12466851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Strausberg R.;
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Mammalia; Butheria; Rodentia;
   Hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The FANTOM Consortium,
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Pred. No. 0.0006;
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Matches 10
                                                                                                                                                                  "Complete genome sequence of the mode coelicolor A3(2).",
Nature 417:141-147(2002).
EMBL; AL939132; CAC16433.1; -.
InterPro; IPR002085; Adh_zn_family.
Pfam; PF00107; adh_zinc; 1.
Complete proteome.
SEQUENCE 317 AA; 31455 MW; 5AB933
                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.

SETRAIN=A3(2) / M145;

MEDLINE=21996410; PubMed=12000953;

MEDLINE=21996410; PubMed=12000953;

MEDLINE=21996410; PubMed=12000953;

MEDLINE=11996410; PubMed=12000953;

MEDLINE=21996410; PubMed=12000953;

MEDLINE=21996410; PubMed=12000953;

MEDLINE=21996410; PubMed=12000953;

MEDLINE=21996410; A., Kieser H., Kieser H., Kieser H., Cardina A., Fraser A., Goble A., Hidalgo J., Horneby T., Howarth S., Cronin A., Fraser A., Goble A., Hidalgo J., Horneby T., Howarth S., Huang C.-H., Klaser T., Larke L., Murphy L., Oliver K., O'Neil S., Huang C.-H., Klaser T., Larke L., Murphy L., Oliver K., O'Neil S., Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S., Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S., Taylor K.

Marren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9F3C2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=97000351; PubMed=8843436;
Redembach M., Kieser H.M., Denapaite D.,
Kinashi H., Hopwood D.A.;
"A set of ordered cosmids and a detailed
the 8 Mb Streptomyces coelicolor A3(2) cheel 8 Mb Streptomyces desired and a detailed the 8 Mb Streptomyces coelicolor A3(2) cheel 8 Mb Streptomyces desired and a detailed the 8 Mb Streptomyces coelicolor A3(2) cheel 8 Mb Streptomyces desired and a detailed the 8 Mb Streptomyces coelicolor A3(2) cheel 8 Mb Streptomyces desired and a detailed the 8 Mb Streptomyces desired and a detailed 
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Cerdeno A.M., Parkhill J., I
Submitted (NOV-2000) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. STRAIN=A3(2);
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Saunders D.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Streptomycineae, Streptomycetaceae, NCBI_TaxID=1902;
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Bacteria, Actinobacteria,
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01-MAR-2001 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
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e EMBL/GenBank/DDBJ databases.
                                                                                  Score 9; DB 1; Pred. No. 4.6
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Tvrosine kinase receptor-
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Q18041,
01-NOV-1996
               Caenorhabditis elegans.
Bukaryota; Metazoa; NemataRhabditidae; Peloderinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PRO0109; TYRKINASE.
Prodom; PD000001; Prot kinase; 1.
SMART; SMO0469; HIF; 1.
PROSITE; PS50011; PROTEIN KINASE DOM; 1.
PROSITE; PS00109; PROTEIN KINASE TYR; 1.
Hypothetical protein; ATP-binding; Kinase;
Tyrosine-protein kinase.
SEQUENCE 562 AA; 63406 MW; F366B69F7F84
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"Direct Submission.";
Submitted (JUN-2001)
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Submitted (DEC-1995)
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STRAIN=Bristol N2;
MEDLINE=99069613;
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Bukaryota; Metazoa; Nematoda; Chromadorea;
Rhabditidae; Peloderinae; Caenorhabditis.
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01-MAR-2003
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STRAIN-Bristol N2;
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HSSP; P11362; 1FGK.
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STRAIN-Bristol N2;
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Science 282:2012-2018(1998).
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                                                                                               3MBLrel. 12, Created)
3MBLrel. 12, Last sequence update)
3MBLrel. 23, Last annotation updat
receptor-related protein RYK prec
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                    caenorhabditis.
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RN (1)
RP SEQUENCE PROM N.A.
RC STRAIN=Bristol N2;
RX MEDIINE=99167506; PubMed=10066802;
RX MEDIINE=9167506; PubMed=10066802;
RX MEDIINE=9167506; PubMed=10066802;
RX MEDIINE=91676; PubMed=10066802;
RX Treated to tyrosine kinases (Ryk).";
RI Treated to tyrosine kinases (Ryk).";
RI Treated to tyrosine kinases (Ryk).";
RI TREATETO; PRO01219; PROTE_kinase.
DR InterPro; PRO01219; PROTE_kinase.
DR InterPro; PRO0125; MIF; 1.
DR Pfam; PP00069; Pkinase; 1.
DR Pfam; PP00069; Pkinase; 1.
DR PFAM; PP00069; PROTEIN KINASE DOW; 1.
DR PROSITE; PS00101; PROTEIN KINASE TYR; 1.
DR PROSITE; PS00101; PROTEIN KINASE TRECEPTOR-RELATED PROTEIN.
DR PROSITE; PS00101; PROTEIN KINASE TRECEPTOR-RELATED PROTEIN.
DR PROSITE; PS00101; PROTEIN KINASE TRECEPTOR-RELATED PROTEIN.
DR PROSITE; PS0010; PROTEIN KINASE TYR; 1.
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RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altechul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Parmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Parmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Raha S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
RA Willalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R. A.,
RA Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green B.D., Dickeon M.C.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.B., Jones S.J.M., Marra M.A.,
"Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences."
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Best Local
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SEQUENCE FROM N.A.
TISSUE=Cervix, and
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SMANT; SM00220; S_TKC; 1.
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Pfam; PF00069; pkinase, 1
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SIMILARITY: Contains 1 protein kinase domain.
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ER -> DREK (IN REF. 1).
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Q8K4K2; Q921E7;

PRT;

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RESULT 3
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Best Local
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-!- FUNCTION: May play an important role in a common pathway leading to programmed neuronal cell death. Does not appear to function in the programmed death of non-neuronal cells. May serve as an endogenous antagonist competing for substrate with functional kinases that act to promote neuronal cell survival.

-!- TISSUE SPECIFICITY: Detected only in the lung. Not detected in the heart, brain, spleen, liver, skeletal muscle, kidney and testis.

-!- INDUCTION: Expression induced during programmed cell death evoked in neuronal cells by NGP-depletion.

-!- SIMILARITY: Contains 1 protein kinase domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM TISSUE=Neuron
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Mammalia; Butheria; Rodentia;
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Neuronal cell death inducible
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RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baidarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Balake J.A., Bradt D., Brusic V.Chochia C., Corbani L.E., Cousins S.,
RA Blake J.A., Bradt D., Brusic V., Chochia C., Corbani L.E., Cousins S.,
RA Balake J.A., Bradt D., Brusic V., Chochia C., Corbani L.E., Cousins S.,
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RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
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RA Kanai A., Schneider C., Semple C.A., Sectou M., Shimada K.,
RA Nagshima T., Numata K., Okido T., Pavan W.J., Partea G., Pesole G.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sultana R., Taylor M.S., Teaddale R.D., Tomita M.,
RA Wilming L.G., Wynshaw-Boris A., Yangi Sawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zhmmer A., Carninci P., Hayatsu N.,
RA Hirozane Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Mirai A., Hashirume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Mirai A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
Panai Anjayashi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Wanai S., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
Panai Anjayashi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Wanai S., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
Panai R., Wanai Y., Rangi P., Panai Y., Panai Y., Lander E.S., Rogers J.,
                     RX MRDLINB=22388257; PubMed=12477932;

RA Strausberg R.L., Peingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altechul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Btopleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,

RA Btopleton M., Josham B., Toshiyuki S., Carninci P., Prange C.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Hotriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

RA Generation and initial analysis of more than 15,000 full-length

Thuman and mouse cDNA sequences .,

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28-PEB-2003
28-PEB-2003
15-SEP-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Analysis of the mouse transcriptome based on 60,770 full-length cDNAs.";
Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=22354683;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kiss-Toth E., Dempsey Bagstaff S.M., Wyllie
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Mammalia; Eutheria;
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(Rel. 42,
play an
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Rodentia;

    Created)
    Last sequence update)
    Last annotation update)
    inducible putative kinase

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D.H., Harte M.,
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Sciurognathi; Muridae
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common
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L.A.J., Qwa
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; Murinae; Mus
pathway leading
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, Kiyosawa H.,
C., Gojobori T.,
ush J.,
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RESULT 4
HUNB DROMU
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Matches 22
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16-OCT-2001 (Rel. 40, Created)

16-OCT-2001 (Rel. 40, Last sequ

15-SEP-2003 (Rel. 42, Last anno

15-SEP-2003 (Fragments).
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CONFLICT
CONFLICT
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EMBL; AK089931; BAC41002.1; -.
EMBL; BC012955; AAH12955.1; -.
InterPro; IPR000719; Prot_kinase.
InterPro; IPR002290; Ser thr_pkinase.
Pfam; PF00069; pkinase; Z.
This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outset the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in
                                                                                                                                                        Baker R.H., Desalle R.;
"Multiple sources of character information Hawaiian Drosophilids.";
                                                                                                                                                                                                                                                   Drosophila mulleri (Fruit fly).

Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygo
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                вувс.
                                                                                                                                                                                                         SEQUENCE FROM N.A.
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ProDom; PD000001; Prot_kinase;
SMART; SM00220; S_TKC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM
                                                                                                                                                                                                                                    NCBI_TaxID=7231;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE;
                                                                                   It. Biol. 46:654-673(1997).

PINCTION: GAP CLASS SEGMENTATION PROTEIN OF HEAD STRUCTURES (BY SIMILARITY).

SUBCELLULAR LOCATION: Nuclear (By similar SIMILARITY).

SIMILARITY: BELONGS TO THE HUNCHBACK FAMI
                                                                       FINGER PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     to programmed neuronal cell death. Does not appear to function the programmed death of non-neuronal cells. May serve as an endogenous antagonist competing for substrate with functional kinases that act to promote neuronal cell survival (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY: Contains 1 protein kinase domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          213
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157
219
239
301
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Pred. No.
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5 -> P (IN REF. 3).

K -> T (IN REF. 1).

MISSING (IN REF. 3).

SERLVALGILLHPWLREDHGRVSPPQSDRREMDQVVPDGPQ
LERAEEGEVGLYG -> CRATCGPGNPLASLVERGSRPSLS
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                                                                                     ear (By similarity).
HUNCHBACK FAMILY OF
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                                                                                                                                                                                                                                                                                                                                                                                                       174
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                             a collaboration -
MBL outstation -
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RESULT 5
PAGG H
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15-SEP-2003
15-SEP-2003
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Q9BYG4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Noda Y., Takeya R., Ohno S., Naito S., I "Human homologues of the Caenorhabditis PAR6 as an adaptor that links the small atypical protein kinase C.", Genes Cells 6:107-119(2001).
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Metal-binding; DNA-binding; Repeat;
NON_TER 1 1
NON_CONS 93 94
NON_TER 174 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=20394296; PubMed=10934474; Joberty G., Petersen C., Gao L., Macara "The cell-polarity protein Paré links Pe C to Cdc42.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa;
Mammalia; Eutheria;
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EMBL; U93015; AAC03263.1; -.
FlyBase; FBgn0023760; Dmul\hb.
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PARD6G OR PAR6G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PubMed=11260256;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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                                                             edmilarity).
SIMILARITY: Belongs to the PAR6 family.
SIMILARITY: Contains 1 pseudo-CRIB domain.
SIMILARITY: Contains 1 PDZ/DHR domain.
                                                                                                                                                 SUBDRIT: Interacts with PARD3 (Probable). In forms of CDC42, ARHQ/TC10 and RAC1. Interact part of PRKCI and PRKCZ.
SUBCELLULAR LOCATION: CZ-toplasmic (Probable)
TISSUB SPECIFICITY: Widely expressed, with a fetal and adult kidney.
DOWAIN: The pseudo-CRIB domain together with required for the interaction with Rho small
                                                                                                                                                                                                                                                                                                                                                         . Cell Biol. 2:531-539(2000).

FUNCTION: Adapter protein involved in asymetrical cell division and cell polarization processes. May play a role in the formation of epithelial tight junctions. The PARD6-PARD3 complex links GTP-bound Rho small GTPases to atypical protein kinase C proteins (By
                                                                                                                                                                                                                                                                                                                                         eimilarity).
SWISS-PROT entry is copyright. It is produced through a case the Swiss Institute of Bioinformatics and the EMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HUMAN
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8; Conserv
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93
174
174 AA;
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(Rel. 42, Last sequence up
(Rel. 42, Last annotation
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Primates;
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s elegans cell pol
l GTPases Rac and
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RESULT 6
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InterPro; IPR001478; PDZ.
Pfam; PP00595; PDZ; 1.
SMART; SM00266; PB1; 1.
SMART; SM00228; PDZ; 1.
PR0SITB; PS50106; PDZ; 1.
Cell Cycle; Cell division; Tight
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NRKA_TRYBB
Q08942;
                                                                                                                                                                                     EMBL; L03778; AAB59252.1;
PIR; T11854; T11854.
HSSP; Q63450; 1A06.
                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a c between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                              "A Trypanosoma brucel gene family encoding protein catalytic domains structurally related to Nekl and Mol. Biochem. Parasitol. 59:111-122(1993).

-I- CATALYTIC ACTIVITY: ATP + a protein = ADP 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN-EATRO 164 / Isolate ISTAR1;
MEDLINE-93295429; PubMed-8515773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Trypanosoma brucei brucei.
Bukaryota; Euglenozoa; Kin
NCBI_TaxID=5702;
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DOMAIN
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16-OCT-2001
                                                                                                                                                                InterPro,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gale M.J. Jr., Parsons M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Putative serine/threonine-protein kinase A (BC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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                                                                                               IPR001849; PH.
IPR000719; Prot kinase.
IPR002290; Ser thr pkinase.
IPR001245; Tyr pkinase.
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Pred. No. 4.7;
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Pfam; PP00169; PH; 1.
Pfam; PP00069; PH; 1.
Pfam; PP00069; Pxinase; 1.
PRINTS; PR00109; TYRKINASE.
ProDom; PD000001; Prot_kinase;
SMART; SM00233; PH: 1

Prot_kinase;

InterPro; InterPro;

nterPro;

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RESULT TO SEE TO
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R PROSITE; PS00100; PROTEIN_KINASE_ST; 1.

R PROSITE; PS00108; PROTEIN_KINASE_DOM; 1.

R PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.

R PROSITE; PS50003; PH_DOWAIN; 1.

R PROSITE; PS50001; PROTEIN_KINASE; PSTORE ATP-binding.

R PROSITE; PS50010; PROTEIN_KINASE; PSTORE ATP-binding.

R PROSITE; PS50010; PROTEIN_KINASE, PSTORE ATP-binding.

R PROSITE; PS50010; PROTEIN_KINASE_DOM; 1.

R PROSITE; PS50010; PROTEIN_KINASE_TOM; 1.

R PROSITE; PS50010; PROTEIN_KINASE_TOM; 1.

R PROSITE; PS50010; PROTEIN_KINASE_TOM; 1.

R PROSITE; PS50010; PROTEIN_KINASE_T
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Best Local
SMART; SM00233; PH; 1.

SMART; SM00220; S TKC; 1.

PROSITE; PS00107; PROTEIN KINASE ATP; PALSE NEG.

PROSITE; PS00108; PROTEIN KINASE ST; 1.

PROSITE; PS50011; PROTEIN KINASE DOM; 1.

PROSITE; PS50003; PH DOMAÏN; 1.

Transferase; Serine/Threonine-protein kinase; ATP-binding.

DOMAIN 20 279 PROTEIN KINASE.
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Q03428;
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InterPro; IPR001849; PH.
InterPro; IPR007719; Prot_kinase.
InterPro; IPR002290; Ser_thr_pkinase.
InterPro; IPR001245; Tyr_pkinase.
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-I- CATALYTIC ACTIVITY: ATP + a protein = ADP + a protein = ADP
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Pfam, PF00069, pkinase; 1.
PRINTS, PR00109, TYRKINASE.
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NCBI_TaxID=5702;
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(Rel. 33, Last sequence update)
(Rel. 40, Last annotation update)
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EMBL; Z28052; CAA8189.1; ALT_INIT.
SGD; S00072243; YKL053C-A.
GO; GO:0007005; P:mitochondrion organization and biogenesis;
Pfam; PF05254; UPF0203; 1.
Hypothetical protein.
SEQUENCE 82 AA; 9296 MW; 6D8EA7CDD89FB73E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outse the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for commodified and this statement is not removed. Usage by and for commodified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rasmussen S.W.;

"Sequence of a 28.6 kb region of yeast chromosome XI includes PBA1 and TOA2 genes, an open reading frame (ORP) similar to a translationally controlled tumour protein, one ORF containing also found in plant storage proteins and 13 ORFs with weak or homology to known proteins.";

Yeast 10:863-868(1994).

-I- SIMILARITY: BRLONGS TO THE UPPO203 (15E1.1) FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FRB-2003 (Rel. 41, Last annotation update)
Hypothetical 9.3 kDa protein in OAR1-CSE4 intergenic region
YKL053C-A.
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Bukaryota; Pungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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or send an email to license@isb-sib.ch).
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STRAIN=S288c;
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                                                                                                                                                                                                                                     Early E3B 10.4 kDa protein Human adenovirus type 7.
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Pfam; PF03376; Adeno_E3B; 1.
ProDom; PD006617; Adeno E3B; 1.
Early protein; Transmembrane; S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entities requires a license agreement (S or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
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Human adenovirus
Viruses, dsDNA vi
SEQUENCE PROM N.A.
STRAIN=87-922;
                                                        MEDLINE=89073758; PubMed=2849239;
Hong J.S., Mullis K.G., Engler J.A.;
"Characterization of the early region
Virology 167:545-553(1988).
                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                           NCBI_TaxID=10519;
                                                                                                                                                                                                                      Viruses;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         - I- SIMILARITY: TO EQUIVALENT PROTEIN IN OTHER ADENOVIRUSES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tollefson A.E., Krajsci P., Yei S.,
"A 10,400-molecular-weight membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=90112650;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=87219876; PubMed=3582978;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FUNCTION: DOWN-REGULATES THE SUBCELLULAR LOCATION: Type I
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7; Conserv
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                                                                                                                                                                                                                                                         precursor.
                                                                                                                                                                                                                  RNA stage; Adenoviridae; Mastadenovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           e; Signal; Endoplasmic r
BY SIMILARITY
BJB PROTEIN
LUMENAL (POTENTIAL)
POTENTIAL.
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Pred.
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10F5281008DB2C41 CRC64;
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9 NO.
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                MERT PSEAE
P04140;
01-NOV-1986
01-NOV-1986
01-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHAIN
DOMAIN
TRANSMEM
DOMAIN
SEQUENCE
                                                                                                      TRANSPOSON-Th501;

MEDLINE-85014891; PubMed=6091128;

Misra T.K., Brown N.L., Fritzinger D.C., Pridmore R.D., Barnes W.M.

Haberstroh L., Silver S.;

Haberstroh L., Silver S.;

"Mercuric ion-resistance operons of plasmid R100 and transposon

"Th501: the beginning of the operon including the regulatory region
and the first two structural genes.";

Proc. Natl. Acad. Sci. U.S.A. 81:5975-5979(1984).

-I- FUNCTION: INVOLVED IN MERCURIC TRANSPORT. PASSES A HG(2+) ION

FROM THE PERIPLASMIC MERP PROTEIN TO THE MERCURIC REDUCTASE
between the Swiss Institute of Bioinformatthe European Bioinformatics Institute. Thuse by non-profit institutions as long modified and this statement is not removed
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kajon A.B., Wadell G.;
Submitted (APR-1995) to the EMBL/GenBank/DDBJ databases
-!- FUNCTION: DOWN-REGULATES THE EGF RECEPTOR.
-!- SUBCELLULAR LOCATION: Type I membrane protein. Endo
                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                       PSEAE
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Pfam, PF03376, Adeno E3B, I
ProDom, PD006617, Adeno E3B
Early protein, Transmembran
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; M23696; AAA53251.1; -.
EMBL; Z48954; CAA88813.1; -.
PIR; C31830; ERAD27.
PIR; G31830; ERAD77.
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                                                                                                                                                                                                                                                                                NCBI_TaxID=287;
                                                                                                                                                                                                                                                                                                            Bacteria;
                                                                                                                                                                                                                                                      SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                         Pseudomonas aeruginosa.
                                                                                                                                                                                                                                                                                                 Pseudomonadaceae;
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Buropean Bioinformatics Institute
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                                                                                       SUBCELLULAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SWISS-PROT entry is copyright. It is produced through a collable en the Swiss Institute of Bioinformatics and the EMBL outst Buropean Bioinformatics Institute. There are no restrictions by non-profit institutions as long as its content is in by non-profit institutions as long as its content is in field and this statement is not removed. Usage by and for content in the profit institutions as long as its content is in the content in the content is not removed. Usage by and for content in the content is not removed.
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7; Conserve
                                                                                                                                                                                                                                                                                                                                                                   transport
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(Rel.
(Rel.
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Transmembrane; S
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                                                                                      LOCATION: Integral
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Last sequence update)
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                                                                                                                                                                                                                                                                                                              Gammaproteobacteria;
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(Mercury ion transport
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Pred. No
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CYTOPLASMIC (POTENTIAL)
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                                                                                    membrane protein.
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                  There are no restrictions on ng as its content is in no
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                                                                                                                                                                                                                                                                                                                                                                   protein)
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                                                                                       Inner membrane.
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RESULT 12
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Best Local S
Matches 7
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01-JAN-1990
28-FEB-2003
                                                                                                                      This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restrues by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-s or send an email to license@isb-sib.ch).
InterPro; IPR005864; ATPaseB.
InterPro; IPR002146; ATPaynt_B/B'sub.
Pfam; PP00430; ATP-synt_B; 1.
TIGR07AMs; TIGR071144; ATP synt_b; 1.
Hydrogen ion transport; Transmembrane; CF(0).
TRANSMEM 2 22 POTENTIAL.
                                                                       EMBL, X16050, CAA34177.1, PIR, 806078, S06078. HSSP, P00859, 189U.
                                                                                                                                                                                                                                                                                                                                                                                                              Vibrio alginolyticus.
Bacteria; Proteobacteria;
Vibrionaceae; Vibrio.
                                                                                                                                                                                                                                                                                                Krumholz L.R., Esser U., Simoni R.D.;
"Nucleotide sequence of the unc operon of Vibrio alginolyticus.";
Nucleic Acids Res. 17.7993-7994 (1989).
-I- CATALYTIC ACTIVITY: ATP + H(2)O + H(+)(In) = ADP + phosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATP synthase B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; Z00027; CAA77321.1;
EMBL; K02503; AAA27433.1;
PIR; A04457; QQPSHT.
                                                                                                                                                                                                                                                                                                                                                  MEDLINE=90016889; PubMed=2529481;
                                                                                                                                                                                                                                                                                                                                                               STRAIN=138-2;
                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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                                                                                                                                                                                                                                                         H(+) (Out).
SUBUNIT: F-TYPE ATPASES HAVE 2 COMPONENTS,
CORE - AND CF(0) - THE MEMBRANE PROTON CHAP
                                                                                                                                                                                                                       CORE - AND CP(0) - THE MEMBRANE PROTON CHANNEL. C
SUBUNITS: ALPHA(3), BETA(3), PAMPA(1), DELTA(1),
HAS THREE MAIN SUBUNITS: A, B AND C.
SIMILARITY: BELONGS TO THE ATPASE B CHAIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VIBAL
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7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    411; MerT; 1.
Transposable element; Mercuric resistance; Inner membrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2.0%;
nilarity 100.0%;
Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      44
94
24
25
76
82
                                                                                                                                                                                                                                                                                                                                                                                                                                                              (Rel. 13,
(Rel. 13,
(Rel. 41,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        $
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Transmembrane.
36 POT
64 POT
114 POT
124 HG(
25 HG(
76 HG(
82 HG()
82 HG()
82 HG()
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
(EC 3.6.3.14).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
                                                                                                                                                                                                                                                                                                                                                                                                                           Gammaproteobacteria; Vibrionales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       score 7; DB 1; Pred. No. 17; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL.
POTENTIAL.
HG(2+) (POT
HG(2+) (POT
HG(2+) (POT
HG(2+) (POT
HG(2+) (POT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL.
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(POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           156
                                                                                                                                    (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ζ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
                                                                                                                                                                                                                                                CP(1) - THE CATALYTIC NNEL. CP(1) HAS FIVE TA(1), EPSILON(1). CP(0)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indele
                                                                                                                                                                      restrictions
                                                                                                                                                  and
                                                                                                                                                                                    IBMB
                                                                                                                                                                                              a collaboration
                                                                                                                                                 for
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                                                                                                                                                                                     outstation
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RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                 RC STRAIN-ATCC 33913 / NCPPB 528;

RM MEDINING-2022145; PubMed=12024217;

RM MEDINING-2022145; PubMed=12024217;

RA da Silva A.C.R., Ferro J.A., Reinach F.C., Camargo L.R., Almedda N.F.,

RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.R.A.,

RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almedda N.F.,

RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.R.,

RA Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorry H.,

RA Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorry H.,

RA Pormighieri B.F., Franco M.C., Greggio C.C., Ferro M.I.T.,

RA Pormighieri B.F., Franco M.C., Greggio C.C., Forber A.M. I.T.,

RA Astsuyama A.M., Kishi L.T., Leite R.P., Lemos B.G.M., Lemos M.V.F.,

RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos B.G.M., Lemos M.V.F.,

RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos B.G.M., Lemos M.V.F.,

RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos B.G.M., Lemos M.V.F.,

RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos B.G.M., Lemos M.V.F.,

RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos B.G.M., Lemos M.V.F.,

RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos B.G.M., Lemos M.V.F.,

RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos B.G.M., Monn D.H.,

RA Formighieri B.C., Medanis J., Menck C.F. M., Myski C.Y., Moon D.H.,

RA Alvest L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,

RA Apinola L.A.F., Takita M.A., Tamura R.E., Teixeira B.C., Tezza R.I.D.,

RA Frindade dos Santos M., Truffi D., Tsai S.M., White F.F.,

RA Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira B.C., Tezza R.I.D.,

RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,

RA Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira B.C., Tezza R.I.D.,

RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,

RA Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira M.C., Oliveira W.t.,

RA Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira M.C., Oliveira W.t.,

RA Spinola L.A.F., Takita M.A., Tamura S.E., Teixeira M.C.,

RA Spinola L.A.F., Takita M.A., Tamura R.E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local &
Matches 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28-PBB-2003 (Rel. 41, Las
28-PBB-2003 (Rel. 41, Las
Sec-independent protein t
TATB OR XCC4092.
                                                                                          HAMAP, MF 0023); -; 1.
InterPro; IPR003369; MttA Hcf106.
InterPro; IPR003998; TatB.
Pfam; PP02416; MtA Hcf106; 1.
                                                                                                                                                                                                                                                                                                                                     This SWI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TATB XANCP
Q8P3H9;
TIGREAMS; TIGRO1410; tatB; 1.
Transport; Protein transport; Translocation;
Inner membrane; Complete proteome.
TRANSMEM 1 21 POTENTIAL.
                                                                                                                                                                                                                                entities requires a license agreement or send an email to license@isb-sib.cl
                                                                                                                                                                                    EMBL, AE012532; AAM43313.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                 PRINTS; PR01506; TATEPROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kanthomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CBI_TaxID=340;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (anthomonadaceae; Xanthomonae.
                                                                                                                                                                                                                                             s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation. Buropean Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way ified and this statement is not removed. Usage by and for commercial ities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                  SUBCELLULAR
SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           342
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                                                                                                                                                                                                                                  an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
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roteobacteria; Gammaproteobacteria;
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                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: Inner-membrane bounded by the tath family.
                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    93
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2.0%; Score 7;
100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 translocase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB . 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       update)
                                                                                                                                                                                                                                                                                                                                                                                                                      bound (Probable).
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CTP1_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matchee
                                                                                                                                                                                      EMBL; U43033; AAD12173.1; -.
EMBL; U43031; AAD12173.1; JOINED.
EMBL; U43032; AAD12173.1; JOINED.
EMBL; U43032; AAD12173.1; -.
EMBL; U43030; AAAB5229.1; -.
PIR; G02312; G02312.
Genew; HGNC:2499; CTF1.
                                                                                                                                                                                                                                                                               the Buropean Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                binding activities, and chromosomal Cytokine 8:183-189(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=96429882; PubMed=8833032;
Pennica D., Swanson T.A., Shaw K.J.,
Beatty B.G., Wood W.I.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1997 (Rel. 35,
01-NOV-1997 (Rel. 35,
28-PEB-2003 (Rel. 41,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                  <del>: :</del>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota, Metazoa;
Mammalia, Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cardiotrophin-1
                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                            Thie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-Heart
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                    GO:0005576; C:extracellular, TAS.
GO:0005146; F:leukemia inhibitory factor
GO:000533; F:cell proliferation, TAS.
GO:0007267; P:cell-cell signaling, TAS.
GO:0007317; P:muscle development; TAS.
GO:000739; F:neurogeneesi; TAS.
GO:000739; F:positive regulation of cell
                                                                                                                                                                                                                                                                                                                                                                                                        PUNCTION: INDUCES CARDIAC MYOCYTE HYPERTROPHY IN VITRO. BINDS TAND ACTIVATES THE LEUKEMIA INHIBITORY FACTOR RECEPTOR (LIF RECEPTOR)/GP 130 RECEPTOR COMPLEX.

SUBCELLULAR LOCATION: Secreted.

SUBCELLULAR LOCATION: Secreted.

TISSUB SPECIFICITY: HIGHLY EXPRESSED IN HEART, SKELETAL MUSCLE, PROSTATE AND OVARY. LOWER LEVELS IN LUNG, KIDNEY, PANCREAS, THYMUS, TESTIS AND SMALL INTESTINB. LITTLE OR NO EXPRESSION IN BRAIN, PLACENTA, LIVER, SPLEEN, COLON OR PERIPHERAL BLOOD IN THE COLORD.
                                                                                                                                                                                                                                                                                                                                                                                   LEUKOCYTES.
SIMILARITY: BELONGS TO THE IL-6
                                                                                                                                                                                                                                                                                                                                               SWISS-PROT entry is copyright. It is produced through sen the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
7, Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATPLAAP 118
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                                                             Polymorphism
92 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             195
                                    201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chordata;
Primates;
                                      21227
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20929
2.0%;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
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                                    MW;
                                                                                      regulation of cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
Score 7; 1
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 7;
Pred. No.
                                                 A -> T (IN dbSNP:2234933)
/FTId=VAR_014938.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                      0235A7B5745F675F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8DDDDB6F526AD390 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                     SUPERFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene structure, localization.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kuang W.-J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              201
 DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1;
                                                                                                                                                                                                                                                                                             (See http://www.isb-sib.
                                                                                                                                                                                                                                                                                                                    ormatics and the EMBL outst
There are no restrictions
ong as its content is in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ₹
                                                                                                                                                                                                                                                                                                         Usage
            Length 201
                                                                                      proliferation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             <u>,</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 195;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gray C.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       biological
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ALIGNMENTS

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Bubmitted to the BMBL Data Library, November 1995
A;Description: The sequence of C. elegans cosmid 밁 र् A;Description: The sequenc A;Reference number: 218365 A;Accession: T15523 hypothetical protein C16B8.1 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 24-Nov-1999 C;Accession: T15523 RESULT T15523 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Residues: 1-548 <BEN> A;Cross-references: EMBL:U41031; NID:g1098982; PID:g1098983; PIDN:AAA82618.1; CESP:C16 ;Gene: CESP:C16B8.1 ;Introns: 13/1; 53/3; 123/1; 176/2; ;Superfamily: unassigned Ser/Thr or Matches Query Match Best Local Genetics: Local Similarity les 9; Conserva 463 AADVWSLGV 471 241 AADVWSLGV 249 Conservative 100.0%; F ative 0; 2.5%; Score 9; DB 2 1; Pred. No. 1.2 0; Mismatches 200/1; 229/3; 255/1; 371/1; 466/3; 512/2 Tyr-specific protein kinases; protein kin DB 2; C16B8 . Length 548; Indels 0 Gapa kinase 0

RESULT A95405

Accession: A95405

R.Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, P.; Bo.; Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K. Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001

A.Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium melil A; Reference number: A95262; MUID:21396509; PMID:11481432

A; Accession: A95405

A; Accession: A95405

A; Status: preliminary
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A; Residues: 1-190 < KUR>
A; Cross-references: GB:AB006469; PIDN:AAK65803.1; PID:914524305; GSPDB:GN00165

A; Cross-references: GB:AB006469; PIDN:AAK65803.1; PID:914524305; GSPDB:GN00165

A; Experimental source: strain 1021, megaphasmid pSyma
A; Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Huble pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.
D:: Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001

A; Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaur hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Kiss, E.; Komp, C.; Lelaur

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A,Title: The composite genome of the legume symbiont Sinorhizobium meliloti. A;Reference number: A96039; MUID:21368234; PMID:11474104
A;Contents: annotation
C;Genetics:
A;Gene: SMa2099
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Mol. Biochem. Parasitol. 59, 111-122, 1993
Mol. Biochem. Parasitol. 59, 111-122, 1993
A/Title: Trypanosoma brucei gene family encoding protein kinases with catalytic domains A/Title: Trypanosoma brucei gene family encoding protein kinases with catalytic domains A/Title: Trypanosoma brucei gene family encoding protein kinases with catalytic domains A/Title: Trypanosoma brucei gene family encoding protein kinases with catalytic domains A/Title: Trypanosoma brucei gene family encoding protein kinases with catalytic domains A/Title: Trypanosoma brucei gene family encoding protein kinases with catalytic domains A/Title: Trypanosoma brucei gene family encoding protein kinases with catalytic domains A/Title: Trypanosoma brucei gene family encoding protein kinases with catalytic domains A/Title: Trypanosoma brucei gene family encoding protein kinases with catalytic domains A/Title: Trypanosoma brucei gene family encoding protein kinases with catalytic domains A/Title: Trypanosoma brucei gene family encoding protein kinases with catalytic domains A/Title: Trypanosoma brucei gene family encoding protein kinases with catalytic domains A/Title: Trypanosoma brucei gene family encoding protein kinases with catalytic domains A/Title: Trypanosoma brucein encoding protein kinases with catalytic domains and catal
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C;Accession: T11854
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A,Molecule type: DNA
A,Residues 1-725 <8TO>
A,Cross-references: GB:AE004729; GB:AE004091; NID:g9949143; PIDN:AAG06436.1; GSPDB:GN00:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ristover, C.K.; Pham, X.O.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Lory, S.; Olson, M.V. Mature 406, 959-964, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          conserved hypothetical protein PA3048 [imported] - Pseudomonas aeruginosa (strain C;Species: Pseudomonas aeruginosa C;Dsecies: Pseudomonas aeruginosa C;Dste: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000 C;Accession: A83266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Note: nrkA
C;Superfamily: unassigned Ser/Thr or
C;Keywords: ATP; phosphotransferase
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A,Molecule type: mRNA
A,Residues: 1-431 <GAL>
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Best Local
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Similarity 100.0%;
8; Conservarion
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                                                                                                              Conservative
                                                                                                                                      2.2%;
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Larbig,
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K.; Lim,
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C;Accession: H44057
R;Mei, Y.P.; Wadell, G.
Virology 191, 125-133, 1992
A;Title: The nucleotide sequence of adenovirus type 11 early 3
A;Reference number: A44057; MUID:93033102; PMID:1413499
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                                                                                                                                early B3 10.3K protein - human adenovirus 11 (strain BC34) (fragment) C;Species: Mastadenovirus h11 (human adenovirus 11) C;Datc: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 12-Ap
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A;Status: preliminary; translated i
A;Status: DNA
A;Molecule type: DNA
A;Residues: 1-33 <OLL>
A;Cross-references: EMBL:AL049573;
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T36211 probable excisionase - Streptomyces coelicolor (fragment)
C;Species: Streptomyces coelicolor
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_
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C;Superfamily: Bacillus probable copper-transporting
C;Keywords: hydrolase
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A; Rolecule type: DNA
A; Residues: 1-813 < KUR>
A; Cross-references: GB: AE008917; PIDN: AAL51235.1; PID: 917981923; GSPDB: GN00190
A; Cross-references: Strain 16M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Accession: T36211
R;Oliver, K.; Harris, D.; Bentley, S.D.; Parkhill, submitted to the EMBL Data Library, March 1999
A;Reference number: Z21577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2.2%; Score 8; DB:
100.0%; Pred. No. 19
tive 0; Mismatches
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A;Molecule type: DNA
A;Residues: 1-72 «KUR»
A;Cross-references: GB:AE008689; PIDN:AAL44866.1; PID:g17742513; GSPDB:GN00187
A;Experimental source: strain C58 (Dupont)
                                                                                                                                                                                                                                    A,Title: The Genome of the Natural Genetic A,Reference number: AB2577; MUID:21608550; A;Accession: AD3056
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R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
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AD3056
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C/Species: Streptomyces coelicolor
C/Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 19-May-2000
C/Accession: T36199
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A;Molecule type: DNA
A;Residues: 1-66 <MEI>
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A;Molecule type: DNA
A;Residues: 1-66 <SAU>
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                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein Atu4065 [imported] - Agrobacterium tumefaciens (strain C58,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Reference number: Z21600
A;Accession: T36199
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Best Local &
Matches
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Best Local Similarity
Matches 7; Conserv
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;Superfamily: adenovirus early E3 10.3K protein
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Baunders, D.C.;
                                                                 Query Match
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Local Similarity 100.0%; F
hee 7; Conservative 0;
                               Local Similarity
les 7; Conserv
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278 YALPAGL 284
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                               2.0%; Score 7; DB:
llarity 100.0%; Pred. No. 21
Conservative 0; Mismatches
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100.0%; Pre
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19,
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                                               DB 2;
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RESULT 12

RRAD27

early R3 10.3K protein - human adenovirus 3

C;Species: Mastadenovirus h3 (human adenovirus 3)

A;Note: host Homo sapiens (man)

C;Date: 31-Mar-1989 #eequence_revision 31-Mar-1989

C;Accession: C31830; H29500
                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: EMBL:Z28054; MIPS:YKL053c-a
A;Accession: 878074
A;Molecule type: DNA
A;Residues: 1-66 <RA2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-86 <RAS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Variety: strain S288C
C;Date: 15-Jan-1999 #sequence revision
C;Accession: S78725; 578074
R;Rasmussen, 8.; von Wettstein, D.
Rspandsted to the Protein Sequence Datal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K. Lancet 357, 125-1240, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein SA1809 [imported] - Staphylococcus aureus (strain N315) C;Species: Staphylococcus aureus C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
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A; Accession: S78725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein YKL053c-a - yeast (Saccharomyces cerevisiae) (Species: Saccharomyces cerevisiae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-80 < KUR>
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100.0%; Pred. No.
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                   #text_change 07-Nov-1997
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R;8ignaes, C.; Akusjaervi, G.; Pettersson, U.
Gene 50, 173-184, 1986
A;Title: Region B3 of human adenoviruses; differences between the oncogenic adenovirus-A;Reference number: A91566; MUID:87219876; PMID:3582978
A;Accession: C31830
                                                                                                                                           hypothetical protein merT - Pseudomonas aeruginosa transposon Tn501
C;Bpecies: Pseudomonas aeruginosa
C;Bate: 04-Dec-1986 #sequence_revision 04-Dec-1986 #text_change 24-Sep-1999
C;Accession: A04457
R;Misra, T.K.; Brown, N.L.; Pritzinger, D.C.; Pridmore, R.D.; Barnes, W.M.; Haberstroh, Proc. Natl. Acad. Sci. U.S.A. 81, 5975-5979, 1984
A;Title: Mercuric ion-resistance operons of plasmid R100 and transposon Tn501: the begin A;Reference number: A03556; MUID:85014891; PMID:6091128
A;Accession: A04457
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ERAD77
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A;Note: the GenBank entry ADREJA (2209908 differs
C;Superfamily: adenovirus early E3 10.3K protein
C;Keywords: early protein; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: EMBL:Z48954; NID:g762955; PIDN:CAA88813.1; PID:g762962
C;Superfamily: adenovirus early E3 10.3K protein
C;Keywords: early protein; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: GB:M23696; NID:g341012; PIDN:AAA53251.1; R;Kajon, A.B.; Wadell, G. submitted to the EMBL Data Library, April 1995 A;Description: Sequence analysis of the E3 region and fiber CA;Reference number: 852798 A;Accession: 852804 A;Accession: 852804 A;Status: preliminary
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A; Residues: 1-91 <8IG>
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Matches 7
                                                ¡Cross-references: GB:Z00027;
¡Genetics:
/Superfamily: merT protein
                                                                                                ,Molecule type: DNA
,Residues: 1-116 <MIS>
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;Residues: 1-91 <HON>
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100.0%; Pred. No.
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100.0%; Pred. No. 26;
                                                                       GB:K00031; GB:K01725; GB:X01297; GB:X03406; NID:g43714;
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Search completed: January 15, Job time: 22 secs

2004, 15:05:54

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R;Klenk, H.P.; Clayton, R.A.; Tomb, J.P.; White, O.; Nelson, K.B.; Ketchum, K.A.; Do.; Pleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, Glodck, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.P.; McDonald, L. Nature 390, 364-370, 1997

Nature 390, 364-370, 1997

A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes Smith, H.O.; Moese, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing arc A;Reference number: A69250; MUID:98049343; PMID:9389475

A;Accession: B69418
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B69418
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                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein AP1347 - Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Date: 05-Dec_1997 #sequence_revision 05-Dec-1997 #text_change 22-Oct-1999
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                                                                                                                                                          A;Cross-references: GB:AE001011; GB:AE000782; NID:g2689334; PIDN:AAB89916.1; PID:g2649
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Best Local Similarity 100.0%; Pred. No.
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7; Conservative
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                                                                            Score 7; DB 2
; Pred. No. 34;
0; Mismatches
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                                                                                                  DB 2;
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                                                                                                                   Length 123;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                Gaps
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irkness, B.
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Post-processing: Listing first 45 summaries
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Maximum DB seq length: 200000000
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                    Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Published Applications AA:*

1: /cgn2=6/ptodata/2/pubpaa/US07 PUBCOMB.pep:*

2: /cgn2=6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*

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9: /cgn2=6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*

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11: /cgn2=6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*

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13: /cgn2=6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*

14: /cgn2=6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*

15: /cgn2=6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*

16: /cgn2=6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*

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18: /cgn2=6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
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358
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                                                        15 US-10-228-263-2

12 US-10-291-172-394

9 US-09-864-761-45703

12 US-10-291-172-680

12 US-10-291-172-680

15 US-10-156-761-12825

15 US-10-156-761-12825

15 US-10-156-761-13581
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US-09-925-301-1102
US-09-925-301-1367
US-09-925-301-1367
US-09-864-761-45767
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUMMARIES
Sequence 8, Appli
Sequence 102, Ap
Sequence 1167, Ap
Sequence 25767, A
Sequence 45767, A
Sequence 304, Appli
Sequence 45703, A
Sequence 6584, Ap
Sequence 6784, Ap
Sequence 12825, A
Sequence 12835, A
Sequence 5125, Ap
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Sequence 623,	12 US-09-882-171-623	232	7 2.0	U 4
Sequence	US-10-	214	7 2.0	43
	-10-369-493-	214	7 2.0	
Sequence 6,	S	214	7 2.0	1
ø	10 US-09-515-806-10	214	7 2.0	0
Sequence 4	9 US-09-834-496A-4	212	7 2.0	39
Sequence		201	7 2.0	38
Sequence	15 US-10-107-931-8	201	٠	7
Sequence	12 US-10-407-303-8	201	7 2.0	36
Sequence	US-09-901-257-	201		G
Sequence	10 US-09-896-856-8	201	7 2.0	4
Sequence	US-09-901-540-	201	7 2.0	w
Sequence 14	c	186		N
	15 US-10-156-761-8607	185	٠	_
Sequence 27, Appl	c	176		0
	12 US-10-104-047-2785	170		9
Sequence 211,	11 US-09-984-271-211	160	٠	28
Sequence 4566	12 US-10-108-260A-4566	158	7 2.0	27
	12 US-10-104-047-3610	158		26
Sequence 22,	9 US-09-799-875-22	130	2	ū
Sequence 30,	๘	117	2	4
	12 US-10-264-049-3683	114		23
	11 US-09-764-891-3951	102		22
	US-09-764-891		N	_
Sequence 740,	15 US-10-083-357-740			20
Sequence	12 US-10-029-386-31085		N	19
Sequence 46811	US-09-864-7		2	8
Sequence	12 US-10-029-386-32285	31		17
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ALIGNMENTS

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US-09-799-875-8
Sequence 8, Application US/09799875
Patent No. US20020034780A1
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                                                                                                                                                                                                                                                                                                                                                             ; NUMBER OF SEQ ID NOS: 33
; SOPTWARE: FastSEQ for W1
; SEQ ID NO 8
; SEQ ID NO 8
; LENGTH: 358
; TYPE: PRT
; ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Meyers, Rachel
APPLICANT: Kapeller-Libermann, Rosana
APPLICANT: Williamson, Mark
TITLE OF INVENTION: No. US20020034780)
FILE REFERENCE: 35800/20996
                                                                                                                                                                                                                                        Query Match 76.5%; Score 274; DB 9; LA Best Local Similarity 100.0%; Pred. No. 1.5e-247; Matches 274; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/799,875
CURRENT FILING DATE: 2001-03-06
PRIOR PPLICATION NUMBER: 60/182,059
PRIOR FILING DATE: 2000-02-11
PRIOR APPLICATION NUMBER: 09/659,287
PRIOR FILING DATE: 2000-09-12
                                                                                 145 HSLVRSRHRIPBPEAAVLFRQMATALAHCHQHGLVLRDLKLCRFVFADRBRKKLVLENLB
                                                145 HSLVRSRHRIPEPEAAVLFROMATALAHCHOHGLVLRDLKLCRFVPADRERKKLVLENLE
205 DSCVLTGPDDSLWDKHACPAYVGPEILSSRASYSGKAADVWSLGVALFTMLAGHYPFQDS
                                                                                                                                                                            85 ALHCPTGTEYTCKVYPVQBALAVLEPYARLPPHKHVARPTEVLAGTQLLYAFFTRTHGDM 144
                                                                                                                                             85 ALHCPTGTEYTCKVYPVQEALAVLEPYARLPPHKHVARPTEVLAGTQLLYAFFTRTHGDM
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                                                                                                                                             144
                                             204
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APPLICANT: VITCA, Duke
APPLICANT: Bird, Timothy A.
APPLICANT: Bird, Timothy A.
APPLICANT: Marken, John S.
APPLICANT: Marken, John S.
TITLE OF INVENTION: Human cDNAs Encoding Polypeptides Have TITLE OF INVENTION: Functions
FILE REFERENCE: 2877-US
CURRENT APPLICATION NUMBER: US/10/024,828
CURRENT APPLICATION NUMBER: US/09/509,902A
PRIOR APPLICATION NUMBER: US/09/509,902A
PRIOR FILING DATE: 1999-08-03
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patentin Ver. 2.0
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US-09-925-301-1102
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-024-828-9
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FILE REPERENCE: pA106
CURRENT APPLICATION NUMBER: US/09/925,301
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05882
PRIOR FILING DATE: 2000-03-08
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1694
SOPTWARE: PATENTIN Ver. 2.0
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                                                                                                                                                                                                                           Sequence 1102, Application US/09925301
Patent No. US20020052308A1
GENERAL INFORMATION:
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Best Local
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                                                                                                                                                                                 APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  247
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DSCYLTGPDDSLMDKHACPAYVGPBILSSRASYSGKAADVMSLGVALFTWLAGHYPPQDS 264
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EPVLLFGKIRRGAYALPAGLSAPARCLVRCLLRREPAERLTATGILLHPWLRQD
                                                                                                                                                                                                                                                                                                                                                                                           EPVLLFGKIRRGAYALPAGLSAPARCLVRCLLRREPAERLTATGILLHPWLRQD 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                  DSCVLTGPDDSLWDKHACPAYVGPEILSSRASYSGKAADVWSLGVALFTMLAGHYPFQDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSLVRSRHR I PBPEAAVLFROMATALAHCHOHGLVLRDLKLCRFVFADRERKKLVLBNLB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        65.4%; Score 234; DB 15; 1 ilarity 100.0%; Pred. No. 3.6e-210; Conservative 0; Mismatches 0;
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                                                                                                                                                                                       Antibodies
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; SEQ ID NO 1102
; LENGTH: 23
; TYBE: PRT
; TYBE: PRT
; ORGANISM: Homo sapiens
US-09-925-301-1102
                                                                   ; OTHER INFORMATION: US-09-925-301-1367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins an:
FILE REFERENCE: PA106
CURRENT APPLICATION NUMBER: US/09/925,301
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: FOT/US00/05882
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
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US-09-925-301-1367
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                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 1367
LENGTH: 153
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 58.1%; Score 208; Di
Best Local Similarity 100.0%; Pred. No. 4.:
Matches 208; Conservative 0; Mismatches
   Matches
               Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1367, Application US/09925301 Patent No. US20020052308A1
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OTHER INFORMATION: )
NAMB/KSY: SITE
LOCATION: (142)
OTHER INFORMATION: )
NAMB/KSY: SITE
LOCATION: (143)
OTHER INFORMATION: )
OTHER INFORMATION: )
LOCATION: (152)
LOCATION: (152)
LOCATION: (152)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 1694
                                                                                                                                                                                                                                                                   LOCATION: (138)
OTHER INFORMATION:
NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                      NAME/KEY: SITE
LOCATION: (136)
OTHER INFORMATION: Xaa
                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                        NAMB/KBY: SITE
                                                                                                                                                                                                                                                                                                                                                                                              PBATURB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          331
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                 Similarity
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Conservative
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                                                                                 Xaa equals any of the naturally occurring L-amino acids
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Pred. No.
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Mismatches
                                                                                                                                   of the naturally occurring L-amino acids
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               DB 9; L
9.3e-50;
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                              Length 153
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US-09-864-761-45767
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                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 49117
SOPTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 45767
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CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
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PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
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TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR PILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
                                                                                                                                                                                                                                                                                                                            PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: US 60/234,687
OTHER INFORMATION: MAP TO ACO09486.3
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.93
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 5.2
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.59
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.93
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.93
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.96
OTHER INFORMATION: SWISSPROT HIT: O74536, EVALUE 1.00e-18
                                                                                                                                                                                                 ORGANISM: Homo sapiens
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APPLICATION NUMBER: PCT/US01/00667
FILING DATE: 2001-01-30
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                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 09/608,408
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                                                                                                                                                                                                                                                                                                                                                                                                                     PILING DATE: 2000-09-
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                         Query Match
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CURRENT APPLICATION NUMBER: US/10/228,263
CURRENT FILING DATE: 2002-12-04
PRIOR APPLICATION NUMBER: US 60/330,797
PRIOR FILING DATE: 2001-10-31
PRIOR APPLICATION NUMBER: US 60/314,655
PRIOR APPLICATION NUMBER: US 60/314,655
PRIOR FILING DATE: 2001-08-27
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin version 3.1
SEQ ID NO 2
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Publication No. US20030099985A1

GENERAL INFORMATION:
APPLICANT: LI, Jing
APPLICANT: LI, 
                                                              ORGANISM: Homo US-10-291-172-304
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                                                                                                                                                                        NUMBER OF SE
SEQ ID NO 304
LENGTH: 269
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Hyseq, Inc
TITLE OF INVENTION: No. US20030228584A1e1
FILE REFERENCE: 21272-045
CURRENT APPLICATION UMMBER: US/10/291,172
CURRENT FILING DATE: 2000-11-08
PRIOR APPLICATION NUMBER: 09/693,267
PRIOR PILING DATE: 2000-10-20
                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 09/665,363
PRIOR FILING DATE: 2000-09-19
PRIOR PELICATION NUMBER: 09/616,847
PRIOR FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: 09/596,193
PRIOR FILING DATE: 2000-06-17
PRIOR FILING DATE: 2000-06-17
                                                                                                                                                                                                                                                                                         PRIOR FILING DATE: 2000-03-07
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                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 09/519,705
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                                                                                                                                                                                                                                                          SEQ ID NOS:
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100.0%; Pred. No.
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100.0%; Pred. No. 6.1e-05
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   Length 269;
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RESULT 8
US-09-864-761-45703
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                                   OTHER INFORMATION: M
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CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
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APPLICANT: Chen, Wensheng
TITLE OP INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OP INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ENERAL INFORMATION:
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80FTWARE: Annomex Sequence Listing Engine vers. 1.1
EQ ID NO 45703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR
                                                                                                                                                                     ORGANISM: Homo sapiens
                                                                                                                                                               FBATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: GB 24263.6
FILING DATE: 2000-10-04
APPLICATION NUMBER: US 60/236,359
FILING DATE: 2000-09-27
APPLICATION NUMBER: PCT/US01/00666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 60/180,312
FILING DATE: 2000-02-04
APPLICATION NUMBER: US 60/207,456
PILING DATE: 2000-05-26
                                                                                                                                                                                                                                                                                           PILING DATE: 2000-06-30
APPLICATION NUMBER: US 09/774,203
PILING DATE: 2001-01-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00667
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00664
FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 09/632,366 FILING DATE: 2000-08-03
                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00670
FILING DATE: 2001-01-30
APPLICATION NUMBER: US 60/234,687
                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 2000-09-21
APPLICATION NUMBER: US 09/608,408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: PCT/US01/00662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: PCT/US01/00668
PILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: PCT/US01/00661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: PCT/US01/00663
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: PCT/US01/00665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: PCT/US01/00669
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                MAP TO AC009486.3

EXPERSSED IN LUNG, SIGNAL = 1.2

EXPERSSED IN PLACENTA, SIGNAL = 0.8

EXPRESSED IN ADULT LIVER, SIGNAL = 0.95

EXPRESSED IN PETAL LIVER, SIGNAL = 1

EXPRESSED IN BRAIN, SIGNAL = 0.97

EXPRESSED IN BONE MARROW, SIGNAL = 0.62
    SWISSPROT
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P57058, EVALUE 1.00e-06
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; OTHER INFORMATION: EST_HUMAN HIT: AU127403.1, US-09-864-761-45703
; ORGANISM: Caenorhabditis elegans US-10-369-493-6754
                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 10
US-10-369-493-6754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: Homo mapienm
US-10-291-172-680
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                                                TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 6754
LENGTH: 548
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 752
SEQ ID NO 680
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Publication No. US20030233675A1
GENERAL INFORMATION:
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Best Local
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Best Local
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 09/693,267
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 09/665,363
PRIOR FILING DATE: 2000-09-19
PRIOR APPLICATION NUMBER: 09/616,847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Hyseq, Inc
TITLE OF INVENTION: NO. US20030228584A1el
PILE REFERENCE: 21272-045
CURRENT APPLICATION NUMBER: US/10/291,172
CURRENT FILING DATE: 2000-11-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 09/519,705
PRIOR FILING DATE: 2000-03-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 09/596,193
PRIOR FILING DATE: 2000-06-17
PRIOR APPLICATION NUMBER: 09/574,454
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                                      TYPE: PRT
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Local Similarity 100.0%;
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nes 9; Conserv
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b. US20030228584A1
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100.0%; Pred. No.
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0; Mismatches
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Length 357;

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APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SHAKKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR PILING DATE: 2001-05-05
PRIOR FILING DATE: 2001-05-07
PRIOR FILING DATE: 2001-08-02
NUMBER OP SEQ ID NOS: 15109
SEQ ID NO 13581
LENGTH: 357
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APPLICANT: IKEDA, HARUO
APPLICANT: ISTKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
                                                                                                                                                                                                                                                                                                                                     APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROS
APPLICANT: SHIBA, TADAYOSH
APPLICANT: SAKAKI, YOSHIYU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 13581, Application US/10156761 Publication No. US20030119018A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 12825
LENGTH: 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 2.2%; Score 8; DB: Best Local Similarity 100.0%; Pred. No. 28; Matches 8; Conservative 0; Mismatches
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Best Local
ORGANISM: Streptomyces avermitilis 10-156-761-13581
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CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
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Similarity 100.0%; Pred. No. 9.0
9; Conservative 0; Mismatches
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HORIKAWA, HIROSHI
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o. 28;
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APPLICANT: You, H. Howard

APPLICANT: Xu, H. Howard

TITLE OP INVENTION: Identification of Essential Genes in TITLE OP INVENTION: Prokaryotes

PILE REPERENCE: ELITRA.011A

CURRENT APPLICATION NUMBER: US/09/815,242

CURRENT FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR APPLICATION NUMBER: 60/206,848

PRIOR FILING DATE: 2000-05-23

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR PILING DATE: 2000-05-26

PRIOR PILING DATE: 2000-10-23

PRIOR PILING DATE: 2000-10-23

PRIOR PILING DATE: 2000-10-23

PRIOR PRILING DATE: 2000-10-27

PRIOR PILING DATE: 2000-10-27
RESULT 14
US-10-156-761-9867
US-10-156-761-9867, Application US/10156761
Publication No. US20030119018A1
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                                                                                                                                                                                                                                                                                                                                                      ; TYPE: PRT
; ORGANISM: Pseudomonas
US-09-815-242-5125
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Matches 8
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APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOPTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 5125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
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                                                                                                                                                                  25 GLGLDEAR 32
                                                                                                                                                                                                                                                             8; Conservative (
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Trawick, John D.
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00.0%; Pred. No
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Mismatches
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APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: ISHIKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OP INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262

CURRENT APPLICATION NUMBER: US/10/156,761

GENERAL INFORMATION:

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Sequence 2. Application US/09963959

Patent No. US20020165145A1

Patent No. US20020165145A1

PALEANT INFORMATION:

APPLICANT: Meyers, Rachel A.

TITLE OF INVENTION: 33521, A NOVEL HUMAN GUANINE NUCLEOTIDE EXCHANGE FAMILY MEMBER

TITLE OF INVENTION: AND USES THEREOF

PILE REFERENCE: 10440-095001

CURRENT APPLICATION NUMBER: US/09/963,959

CURRENT APPLICATION NUMBER: US/09/963,959

CURRENT FILING DATE: 2001-09-25

PRIOR APPLICATION NUMBER: 60/235,033

PRIOR APPLICATION NUMBER: 60/235,033

PRIOR PILLING DATE: 2000-09-25

NUMBER OF SEQ ID NOS: 13

SOPTWARE: PastSEQ for Windows Version 4.0

SEQ ID NO 2

LENGTH: 1701

TYPE: PRT

ORGANISM: Homo sapiens

US-09-963-959-2
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PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 9867
LENGTH: 1352
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Search completed: January 15, 2004, 15:11:57 Job time: 38 BecB
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US-09-963-959-2
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                                                                                                                                                                                   Query Match 2.2%; Score 8; DB 10; L Best Local Similarity 100.0%; Pred. No. 2.2e+02; Matches 8; Conservative 0; Mismatches 0;
                                                                                             388 GSLSRKKR 395
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Perfect score:
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1: | SID81|gcgdata/geneseq/geneseqp-emb1/AA1980.DAT:*
2: | SID81|gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:*
3: | SID81|gcgdata/geneseq/geneseqp-emb1/AA1982.DAT:*
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9: | SID81|gcgdata/geneseq/geneseqp-emb1/AA1987.DAT:*
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11: | SID81|gcgdata/geneseq/geneseqp-emb1/AA1987.DAT:*
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Gapop 60.0 , Gapext 60.0
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Human protein kina Human polypeptide Human polypeptide Peptide JJ503-KS Human cancer assoc Human protein phos Human kinase PKIN-Human NS protein s
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AAM95293	AAM94871	ABB95990	ABP05531	AAU45811	AAM89922	AAM80256	ABP32052	AAM88522	AAU54213	AAM18595	ABB37647	ABG52461	ABG91809	ABB08024	ABB63460	AAU33629	AAU28323	ABG45892	AAM36793	AAM76686	AAM63872	ABB42968	ABG58378	ABB80975	AAU28135	ABP96856	ABG45957	AAM36904	AAM76798	AAM63978	ABB43079	ABG58479	ABG04413	AAB43922	ABB06108
-	Human reproductive	Human testicular a	Human ORFX protein	Propionibacterium			Human ORF1025 prot	Human immune/haema		Peptide #5029 enco	Peptide #5153 enco	Human liver peptid	<u>.</u>			Pseudomonas aerugi	human se	Human peptide enco	le #10		Human brain expres	Q.	Human liver peptid	tribbles ho	Novel human secret	CBPW pro	Human peptide enco	Peptide #10941 enc		brain exp	Peptide #10585 enc	Human liver peptid	Novel human diagno	Human cancer assoc	Human NS protein ø

ALIGNMENTS

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RESULT 1
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ID AAU0
XX AAUC
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    WPI; 2001-343950/36.
N-PSDB; AAS06709.
                                                                                                                                                                                                                                                                                                                           24-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human, protein kinase; PTK; STK; cancer; cardiovascular disease; metabolic disorder; immune related disease; neurological disorder; neurodegenerative disorder; inflammatory disorder; infectious disease; reproductive disorder.
                                                                                                                    Plowman GD,
Flanagan P,
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                                                                                                                                                           Manning G,
                                                                                                                                                       Sudarsanam S,
                                                                                                                                                                Martinez
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ABB06093

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CC encoding protein kinase (PTK and STK) families. The polynucleotides compound the kinase and the polypeptides may be used in the colorest (especially cancers of haematopoistic origin), cardiovascular commune related diseases (e.g. rheumatoid arthritis), neurological commune related diseases (e.g. schizophrenia), neurodegenerative disorders (e.g. disease (e.g. HIV) and reproductive disorders (e.g. sathma), infectious compounds (e.g. HIV) and reproductive disorders (e.g. infertility).

CC disease (e.g. HIV) and reproductive disorders (e.g. infertility).

CC used for gene therapy and as DNA probes in diagnostic assays.

CC of antibodies against the protein kinases and in assays to identify modulators of protein kinase expression and activity.
RRSULT 2
AAAV3890
IID AAAV3
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Matches 274
                                                                                                                                                        paripheral nervous Bystem; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; emyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; druq screening.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAU03501-AAU03557 represent novel human protein kinases #1-57. novel protein kinases have been identified as members of the toor serine/threonine kinase (PTK and STK) families. The polynuc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic acids encoding human kinase polypeptides, useful for preventing diagnosing and/or treating e.g. cancer, immune, cardiovascular and neuronal-associated diseases, and microbial infections -
                                                                                                                                                                                                                                                                                                                                             Human
                                                                                                                                                                                                                                                                                                                                                                                                      22-OCT-2001
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100.0%; Pred. No. 4e.
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WO200153312-A1

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Matches 261; Conserv
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25-APR-2000;
09-JUL-2000;
19-JUL-2000;
03-AUG-2000;
14-8EP-2000;
19-OCT-2000;
                                                                                                                                                                                                                                                                                                                                          The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activity thes such as: Immune system suppression, Activinyinhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and
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Wang
Zhao
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Note: The sequence
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                                                                                                                                                                                                                                                                                                             specification.
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               DGLGLDEAREBEGDREVVLYG
                                           YALPAGUSAPARCIURCIURREPAGRUTATGIUHPMLRQDPMPLAPTRSHUMBAAQVVP
                                                                                          DKHACPAYVGPEILSSRASYSGKAADVWSLGVALFTWLAGHYPPQDSEPVLLFGKIRRGA
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 DGLGLDEARBBEGDREVVLYG
                                                            YALPAGISAPARCIVRCULRREPAERUTATGILLHPWLRQDPMPLAPTRSHLWEAAQVVP
                                                                                                                                            EAAVLFRQMATALAHCHQHGLVLRDLKLCRFVFADRBRKKLVLENLBDSCVLTGPDDSLW
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ilarity 100.0%;
Conservative (
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2000US-0598042.

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Wehrman T,
Goodrich F
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Xu C,
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Pred. No.
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Query Match
Best Local S
Matches 261
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   03-AUG-2000;
14-SEP-2000;
19-OCT-2000;
                                                                                                                                            assays for receptor activity, arthritis and C.N.S disorders.
Note: The sequence data for this patent did
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Wang
                                                                                                       Sequence
                                                                                                                                 specification.
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                                                                                                                                                                                                                                                                                                                                                      Example
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19-JUL-2000;
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Zhou
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VYPVQEALAVLEPYARLPPHKHVARPTEVLAGTQLLYAFFTRTHGDMHSLVRSRHRIPEP
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ilarity 100.0%;
Conservative
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Wehrman T, )
Goodrich R,
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                                                   Score 261; DB 22;
Pred. No. 2e-245;
0; Mismatches 0
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Xu C,
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Ku C, Xue AJ,
Drmanac RT;
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                                                                                                                                             TOT.
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                                                                                                                                                                     leukaemias
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Query Match Best Local S Matches 234

al Similarity 234; Conserv

Conservative

65.4%; St. 100.0%; Pr

Score 234; DB 21; 1; Pred. No. 3.6e-219; 0; Mismatches 0;

Length 360; Indels

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Gape

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RESULT 4
ANY69157
ID ANY6
XX ANY6
AC A
                                            CC The present sequence represents a partial polypeptide which has kinase CC activity. The kinase polymucleotides can be used to express the CC polypeptides, and as probes to identify nucleic acids encoding CC proteins having kinase activity. The kinase polypeptides and controls for peptides and isoelectric focusing markers, and as controls for peptide fragmentation. They also compare a number of therapeutic uses as kinases play a central role in the cellular signal transduction. The polypeptides could also be used to identify binding partner proteins. The polypeptides can also be used as a reagent to identify any proteins that the polypeptide regulates, and could also be used as a reagent to identify any proteins that the polypeptide may also be used for preparation of antibodies. The antibodies can be used in cassays to detect the presence of the protein, and to purify the protein by immunoaffinity chromatography.
   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New human kinase polypeptides and polynucleotides used as weight markers and as controls for peptide fragmentation
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N-PSDB; AAZ61155.
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11-SEP-1998;
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AAC77607 to AAC78448 encode the human cancer associated proteins given in AAB43398 to AAB4239. The proteins can have activities based on the tissues and cells the genes are expressed in. Example of activities include: cytostatic; proliferative; vulnerary; immunomodulator; antishthmatic; antisheumatic; antibacterial; antivities antishfammatory; antithyroid; antishlergic; antibacterial; antiviral; dermatological, neuroprotective; cardiant; thrombolytic; coagulant; nootropic; vasotropic; antipsoriatic and antiangiogenic. The polynucleotides and polypeptides can be used for preventing, treating or ameliorating medical conditions and diagnosing pathological conditions. Polynucleotides, polypeptides, antibodies, agonists and antagonists from the present invention may be used to treat immune disorders by activating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          diagnosis; cytostatic; proliferative; vulnerary; immunosulator; antidiabetic; antiasthmatic; antirheumatic; antiarthritic; antiviral; antiinflammatory; antithyroid; antiallergic; antibacterial; cardiant; dermatological; neuroprotective; thrombolytic; coagulant; nootropic; vasotropic; antipsoriatic; antiangiogenic; gene therapy; inflammation; immune disorder; haematopoietic cell disorder; autoimmune disorder; treaction; graft versus host disease; organ rejection; haemostatic; thrombolytic; cardiovascular disorder; infection; neurological disease; drug screening.
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N-PSDB; AAC77866.
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                       Modified-site
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                                                                                                                                                                                                                                                                                                                                                            kinase
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                                                                                                                                                                                                                                                                                                                                                              domain
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                                                                                                                                                                                                                                                                                                                                                            eignature"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           human;
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RESULT 7
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AC ABB8
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                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence is that of novel human protein phosphatase and kinase protein pPHKP-5, as predicted from Incyre Clone ID No. CC 1271505CB1 (see AAF30480). Tissues that express PPHKP-5 (as a CC fraction of total tissues expressing PPHKP-5) include reproductive (0.288), gastrointestinal (0.212) and haematopoietic or immune (0.192). Diseases or conditions associated with tissues expressing PPHKP-5) include reproductive (0.192). Diseases or conditions associated with tissues expressing PPHKP-5) include C cancer (0.577), inflammation or trauma (0.327) and cell cancer (0.577), inflammation or trauma (0.327) and cell proliferation (0.308). The encoded protein hows homology to rat kinase. The invention provides human PPHKP-1 also provides expression vectors, host cells, antibodies, agonists and antagonists, as well as methods for diagnosing, treating or preventing disorders associated with expression of PPHKP, including gastrointestinal disorders, immune system disorders, neurological disorders and cell proliferative disorders, including cancer.
                                                                                                                                                                                                                                                                                                                                                         Matches 208;
                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local
                                            ABB80976 standard; Protein; 360 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel human protein phosphatase and kinase proteins for diagnosis, treatment and prevention of gastrointestinal, immune system, neurological and cell proliferative disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Yue H,
                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1, Page 88-89, 103pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lu DAM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14-SEP-2000; 2000WO-US25515
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                                                                                                                                                                                                                                                                                                                                                                      Similarity
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                                                                                                                                                                                                                                                    GPDDSLWDKHACPAYVGPEILSSRASYSGKAADVWSLGVALPTMLAGHYPPQDSEPVLLF
                                                                                                                                                                                          GKIRRGAYALPAGLSAPARCLVRCLLRREPAERLTATGILLHPWLRQDPMPLAPTRSHLW
                                                                                                                                                                                                                                                                                          RHRIPEPEAAVLFROMATALAHCHOHGLVLRDLKLCRFVFADRERKKLVLENLEDSCVLT
                                                                                                                                  BAAQVVPDGLGLDBARBBEGDRBVVLYG
                                                                                                                                                                          GKIRRGAYALPAGLSAPARCLVRCLLRREPAERLTATGILLHPWLRQDPWPLAPTRSHLW
                                                                                                                                                                                                                                   GPDDSLWDKHACPAYVGPEILSSRASYSGKAADVWSLGVALFTMLAGHYPFQDSEPVLLF
                                                                                                                    EAAQVVPDGLGLDEAREEEGDREVVLYG
                                                                                                                                                                                                                                                                                                                                                                                                                 358 AA;
                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99US-0154141
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/note=
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                                                                                                                                                                                                                                                                                                                                                                    58.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "O-phosphorylated"
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                                                                                                                                                                                                                                                                                                                                                  0,
                                                                                                                                                                                                                                                                                                                                                      Score 208; DB 22; Pred. No. 7.3e-194; 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                       330
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ABB80976;

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196

KKLVLENLEDSCVLTGPDDSLWDKHACPAYVGPEILSSRASYSGKAADVWSLGVALFTML

Indels

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Gaps

0

198

316

RQDPMPLAPTRSHLWEAAQVVPDGLGLDEARBBEGDRBVVLYG

AGHYPFODSEPVLLFGKIRRGAYALPAGLSAPARCLVRCLLRREPABRLTATGILLHPWL

AGHYPPQDSEPVLLFGKIRRGAYALPAGLSAPARCLVRCLLRRBPABRLTATGILLHPWL KKLVLENLEDSCVLTGPDDSLWDKHACPAYVGPBILSSRASYSGKAADVWSLGVALFTML

315 317

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CC also known as stress kinase inhibitor protein (SKIP-1) polypeptide. The CC also known as stress kinase inhibitor protein (SKIP-1) polypeptide. The CC signal in a cell. The polypeptide employed in the method is preferably CC htrb-1, htrb-1 N htrb-1 C, htrb-1 N C, htrb-3 N C. It is also useful for providing htrb agonist activity for CC activating an ERK-mediated signal e.g. AP-1-mediated gene activation signal, an estrogen receptor-mediated gene activation signal, an CC signal, an estrogen receptor-mediated gene activation signal, an CC in a cell. Htrb modulators are useful for modulating AP-1 mediated for induced inflammatory signal in a cell such as tumor necrosis factor (TNP) CC induced inflammatory signal, or an interleukin induced inflammatory compounds are useful for modulating AP-1 mediated CC and in thraspeutics or prophylactics. The htrb proteins are useful for cc signal. htrb proteins are useful in a creating analyor preventing diseases caused CC sporiasis, osteoporosis, diabetic retinopathy, myocardial infarction cc and cancers. The htrb therapeutice are useful for and cancers. The htrb therapeutics are useful for and infarction or autoimmune disorders. The present sequence represents cc the htrb-3 polypeptide.
                                                                                Matches 163;
                                         Query Match
                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel isolated human tribbles homologue-1 polypeptide for inhibiting AP-1-mediated inflammatory signal in a cell, and activating ERK-mediated signal e.g. AP-1-mediated gene activation signal in a cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 10; Fig 11B; 131pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; tribbles; htrb-1; stress kinase inhibitor protein; SKIP-1; AP-1; antifheumatic; antiarthritic; antidiabetic; antipsoriatic; osteopathic; opthalamological; cardiant; cytostatic; haemostatic; immunosuppressive; antiinflammatory; estrogen receptor; fibroblast growth factor; PGF; tumour necrosis factor; TNF; htrb-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-590635/63.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     08-JAN-2001; 2001US-260294P
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                        Local
                        Similarity
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                                                                              360
     Conservative
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45.5%; Score 163; DB 2:
100.0%; Pred. No. 4.8e-1
tive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            M
                                      23;
                                    Length 360;
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RODPMPLAPTRSHLWBAAQVVPDGLGLDBARBEBGDRBVVLYG

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RESULT 9
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Best Local S
Matches 115
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Hafalia A, S)
                                                                                                                                                                                                                                                                                                                                                                                                             isolated human kinase polypeptides useful in the diagnosis, treatment and provention of cancer, immune disorders and disorders affecting growth and development -
                                                                                                                                                                                                                                            The invention provides human kinases (PKIN) and polynucleotides encoding PKIN. The PKIN polypeptides can be expressed using standard recombinant methodology. The PKIN polypeptides, polynucleotides, modulators and specific antibodies are useful in the diagnosis, treatment and prevention of cancer, immune disorders, disorders affecting growth and development, atherosclerosis, and other cardiovascular diseases, and lipid disorders and in the assessment of the effects of exogenous compounds on the expression of nucleic acid sequences of human kinases. The present sequence represents a human PKIN-10 polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17-FEB-2000; 2000US-0183682.
02-MAR-2000; 2000US-0186599.
MAR-2000; 2000US-0188606.
17-MAR-2000; 2000US-0189998.
30-MAR-2000; 2000US-0193851.
                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 115; 126pp; English.
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N-PSDB; AAH76218.
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                                                                                                                        244 VWSLGVALFTMLAGHYPFQDSEPVLLFGKIRRGAYALPAGLSAPARCLVRCLLRREPAER
                                                     269
                                                                               304
                                                                                                                                                                              Similarity
                                                                   LTATGILLHPWLRQDPMPLAPTRSHLWEAAQVVPDGLGLDEARBEEGDREVVLYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Buford N, (A, Shih LL, CA, Lu DAM, CA, Lu DAM, CA, Lal P, W
                                                      LTATGILLHPWLRQDPMPLAPTRSHLWEAAQVVPDGLGLDEAREEEGDREVVLYG
                                                                                                          VWSLGVALFTMLAGHYPFQDSEPVLLFGKIRRGAYALPAGLSAPARCLVRCLLRREPAER
                                                                                                                                                                                                                     323
                                                                                                                                                                 Conservative
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Tribouley (
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                                                                                                                                                                            32.1%; Score 115; DB 23
100.0%; Pred. No. 2.4e-1
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                                                                                                                                                                  Mismatches
                                                                                                                                                                      e 22;
103;
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Burrill JD,
Griffin JA,
                                                                                                                                                                                        Length
                                                                                                                                                               Indels
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D. Marcus GA;
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                                                                                                                                                               Gaps
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vasotropic; antiarteriosclerotic; antiinflammatory; dermatological; ancercic; muscular; antiinfertility; cardiovascular; anticosgulant; antifibrinolytic; hypotension; antiasthmatic; immunomodulator; cardiant; anticonvulsant; antidiabetic; tranquilliser; antidepressant; aeuroleptic; gastrointestinal; virucide; antilicer; cerebroprotective; noctropic; contraceptive; vaccine; gene therapy; cancer; osteoporosis; dystonia; endometriosis; degenerative disease; multiple sclerosis; psoriasis; rheumatoid arthritis; cataract; restenosis; atherosclerosis; glaucoma; inflammation; skin disorder; obesity; muscular dystrophy; AIDS; infertility; cardiovascular disease; congulation disease; hypertension; ischaemia; asthma; immune disease; epilepsy; angina; neurodegeneration; disease; anxiety; depression; schizophrenia; viral disease; stroke;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human NS protein sequence SEQ ID NO:185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alzheimer's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              antiarthritic;
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anti-HIV;

WPI; 2002-155037/20 18-JUL-2000; 2000IL-0137345 15-DEC-2000; 2000IL-0140354 17-JUL-2001; 2001WO-IL00653 24-JAN-2002 WO200206315-A2 COMPUGEN LTD. ABL39747. Freilich S,

One hundred and twenty eight novel nucleic acid sequences, treating and diagnosing e.g. cancer, asthma and Alzheimer's useful for

Claim 6; Page 213-214; 290pp; English.

CC vasotropic, antiarreriosclerotic, antiinflammatory, dermatological, antiarreriosclerotic, muscular, anti-HTV, antiinflammatory, darmatological, cardiovascular, antifibrinolytic, hypotension, antiasthmatic, cardiant, communomodulator, antifibrinolytic, hypotension, antiasthmatic, cardiant, cimmunomodulator, antifibrinolytic, bypotension, antiasthmatic, cardiant, communomodulator, anticonvulsant, antidiabetic, tranquilliser, anticonvulsant, antidiabetic, tranquilliser, anticonvulsant, antidiabetic, tranquilliser, anticonvulsant, antidiabetic, carebroprotective, commontoriosic and contraceptive activities. The NS can be used in vaccines, communication vaccines, communication and be used for treating and contibodies from the present invention can be used for treating and contibodies from the present invention can be used for treating and contibodies, carcar, osteoporosis, rendometriosis, degenerative contisted diseases, dystonia, multiple sclerosis, rheumatoid arthritis, psoriasis, cataracts, restenses, atherosclerosis, inflammation, skin disorders, cataracts, restenses, atherosclerosis, inflammation, skin disorders, contisted by the contisted of the contisted by the cardiovascular contisted by the contisted by the cardiovascular contisted by the contisted by the cardiovascular contisted by ABL19691 to ABL39818 represent novel human nucleic acid sequences encoding the proteins given in ABB06037 to ABB06164. The nuver sequences (NS) can have cytostatic, osteopathic, gynaecological, neuroprotective, antirheumatic, antiarthritic, antipsoriatic, ophthalmological, virucide,

Sequence 278 \$

Query Match Best Local S Matches 83 83; Similarity Conservative 23.2%; Score 83; DB 100.0%; Pred. No. 3. ive 0; Mismatches DB 23; 1 3.1e-72; hes 0; Length 278, Indels 0 Gape

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ABL39691 to ABL39818 represent novel human nucleic acid sequences encoding the proteins given in ABB66037 to ABB66164. The novel sequences (NS) can have cytostatic, osteopathic, Synaecological, neuroprotective, antirheumatic, antiarthritic, antipsoriatic, ophthalmological, virucide, vssotropic, antiarteriosclerotic, antiinflammatory, dermatological, antorectic, muscular, anti-HIV, antiinflammatory, dermatological, anti-coagulant, antifibrinolytic, hypotension, antiasthmatic, cardiant, immunomodulator, anticonvulsant, antidiabetic, tranquilliser, antiulcer, antidepressant, gastrointestinal, aeuroleptic, cerebroprotective, nootropic and contraceptive activities. The NS can be used in vaccines, gene therapy and antisense therapy. Nucleic acids, expression vectors and disgnossing e.g. cancer, osteoporosis, endometriosis, degenerative psoriasis, deseases, dystonia, multiple sclerosis, rheumatoid arthritis, psoriasis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     anorectic; muscular; antiinfertility; cardiovascular; anticoagulant; antifibrinolytic; hypotension; antiasthmatic; immunomodulator; cardiant; anticonvulsant; antidiabetic; tranquilliser; antidepressant; aeuroleptic; gastrointestinal; virucide; antiulcer; cerebroprotective; nootropic; contraceptive; vaccine; gene therapy; cancer; osteoporosis; dystonia; endometriosis; degenerative disease; multiple sclerosis; psoriasis; rheumatoid arthitis; cattaract; restenosis; atherosclerosis; glaucoma; inflammation; skin disorder; obesity; muscular dystrophy; AIDS; infertility; cardiovascular disease; coagulation disease; hypertension; ischaemia, asthma; immune disease; coagulation disease; hypertension; disbetes; anxiety; depression; schizophrenia; viral disease; stroke; gastric ulcer; Alzheimer's disease.
                                                                                                                                                                                                                                                                                                                        One hundred and twenty eight novel nucleic acid treating and diagnosing e.g. cancer, asthma and
                                                                                                                                                                                                                                                                                                                                                                               N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-JUL-2000;
15-DEC-2000;
                                                                                                                                                                                                                                                                                       Claim 6; Page 231-232; 290pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; cytostatic; osteopathic; gynaecological; neuroprotective; antirheumatic; antiarthritic; antipsoriatic; ophthalmological; antivasotropic; antiarteriosclerotic; antiinflammatory; dermatological;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17-JUL-2001; 2001WO-IL00653.
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2000IL-0140354.
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                                                                                                                                                                                                                                                                                                                          and Alzheimer's -
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                                                            and
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RESULT 11
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Best Local
      AAC77607 to AAC78448 encode the human cancer associated proteins given in AAB43398 to AAB44239. The proteins can have activities based on the tissues and cells the genes are expressed in. Example of activities include: cytostatic; proliferative; vulnerary; immunomodulator; antidiabetic; antiasthmatic; antirheumatic; antiarthritic; antiinflammatory; antithyroid; antiallergic; antibacterial; antiviral; dermatological; neuroprotective; cardiant; thrombolytic; coagulant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; cancer associated gene; cancer antigen; detection; cancer; diagnosis; cytostatic; proliferative; vulnerary; immunomodulator; antidiabetic; antiasthmatic; antirheumatic; antiarthritic; antiviral; antiinflammatory; antithyroid; antiallergic; antibacterial; cardiant; dermatological; neuroprotective; thrombolytic; coagulant; nootropic; vasotropic; antipsoriatic; antiangiogenic; gene therapy; inflammation; immune disorder; haematopoietic cell disorder; autoimmune disorder; altergic reaction; graft versus host disease; organ rejection; haematopoietic; cardiovascular disorder; infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cataracts, restenosis, atherosclerosis, inflammation, skin disorders, glaucoma, obesity, muscular dystrophy, AIDS, infertility, cardiovascul disease, coagulation disease, sichaemia, hypertension, asthma, immune disease, epilepsy, angina, neurodegeneration, diabetes, anxiety, depression, schizophrenia, viral disease, gastric ulcers, stroke, Alzheimer's disease and as a contraceptive.
                                                                                                                                     Claim 11;
                                                                                                                                                               Novel isolated nucleic useful for treating or
                                                                                                                                                                                                            WPI; 2000-587533/55.
N-PSDB; AAC78131.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                           Rosen
                                                                                                                                                                                                                                                                                        (HUMA-) HUMAN GENOME
                                                                                                                                                                                                                                                                                                                                                   08-MAR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           neurological
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                                                                                                                                  Page 2031;
                                                                                                                                                                                                                                                           Ruben SM
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                                                                                                                                                                                                                                                                                                                                                   2000WO-US05882.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            disease, drug screening.
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                                                                                                                                  2352pp; English.
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                                                                                                                                                               acids comprising sequences diagnosing e.g. cancer -
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Pred. No.
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3.1e-72;
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vasotropic;

antipsoriatic

antiangiogenic.

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Query Match
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   The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy technique.
                                                                                                                                                                                                                                                                                                                 New isolated polynucleotide and encoded polypeptides, useful diagnostics, forensics, gene mapping, identification of mutat responsible for genetic disorders or other traits and to assebiodiversity -
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DB; AAS68600.
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ilarity 100.0%;
Conservative (
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2000US-0649167.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Liu C,
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                                                                                                                                                                                                                                                    34772; 103pp;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ĭ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene mapping; gene therapy; forensic;
maging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               $
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                                                                                                                                                                                                                                                    English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        . NO.
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5.4e-52;
useful in gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 153;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                      to assess
                                                                                                                                                                                                                                                                                                                                                                                          mutations
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   techniques
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stringency liver. (I)

may c

predicting,

displaying

gene

the for

The invention

The invention relates to a single exon nucleic acid probe (SRNP) (I) for measuring human gene expression in a sample derived from human adult liver, comprising one of 13109 defined nucleotide sequences given in the specification (or complements/ fragments). The probe hybridises at high stringency to a nucleic acid molecule expressed in the human adult

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RESULT 13
ABG58479
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Best Local S
Matches 37
                                                                                                                                                                                                                04-FBB-2000; 2000US-0180312.
26-MAY-2000; 2000US-0207456.
30-JUN-2000; 2000US-0632366.
03-AUG-2000; 2000US-0632366.
21-SBP-2000; 2000US-0234687.
27-SBP-2000; 2000US-0236559.
04-OCT-2000; 2000GB-0024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful in medical disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                  Penn
                                                                                 Claim
                                                                                                      analysing
                                                                                                                                                                                                                                                                                                                                        09-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                                        Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human liver peptide,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABG58479;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABG58479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                30-JAN-2001, 2001WO-US00664
                                                                                                                                                                                                                                                                                                                                                                WO200157273-A2
                                                                                                                                                                                                                                                                                                                                                                                                              Human; liver; cirrhosis; hyperlipoproteinaemia; hypercholesterolaemia; coronary heart disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25-PBB-2003
                                                                                                                                                                                          (MOLE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   restore normal activity of (II) or (). (II) is useful for generating ar
                                                                                                                                          2001-488898/53.
                                                                                                                                                                                                                                                                                                                                                                                       sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      110
                                                                               27;
                                                                                                      genome-derived single exon nucleic sing gene expression in human adult
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28
                                                                                                                                                                                         MOLECULAR DYNAMICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ERPVQKRARSGPQPRLPPCLLPLSPPTAPDRATAVAT 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ERFVQKRARSGPQPRLPPCLLPLSPPTAPDRATAVAT
                                                                               SEQ
                                                                                                                                                                  Hanzel
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                                                                               37127;
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                                                                                                                                                                  Chen
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Pred. No.
                                                                                                  exon nucleic acid phuman adult liver
                                                                                                                                                                   Rank
                                                                                                                                                                                                                                                                                                                                                                                                                                                   37127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
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                                                                               English
                                                                                                                                                                  뮸
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1.3e-27;
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                                                                                                                                                                                                                                                                                                                                                                                                                           hyperlipidaemia,
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RESULT 14
ABB43079
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                            The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a peptide encoded by a single exon nucleic acid probe of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   expression in samples derived from human adult liver. The genes identified may be involved in genetic liver diseases such as cirrhosis, hyperlipiperoteinnemia, hyperlipideemia and hypercholesterolaemia which is associated with coronary heart disease. ABG47348-ABG59930 represent human liver single exon encoded peptides of the invention. Note: The sequence information for this patent does not appear in the printed specification but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                         Sequence
                                                                                                                                                                                                                                 Human genome-derived single exon nucleic acid probes useful analyzing gene expression in human fetal liver -
                                                                                                                                                                                                                                                                                                                                                                                                                               04-FEB-2000;
26-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          04-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABB43079 standard; Peptide; 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                          Claim
                                                                                                                                                                                                                                                                                                        Penn
                                                                                                                                                                                                                                                                                                                                                                         21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                     30-JUN-2000;
03-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; foetal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABB43079;
                                                                                                                                                                                                                                                                                                                                  (MOLE-)
                                                                                                                                                                                                                                                                                                       SG,
                                                                                                                                                                                                                                                                             2001-483447/52.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             236
                                                                                                                                                                                                       27, SEQ ID NO 35714; 639pp + sequence listing;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14;
                                                                                                                                                                                                                                                                                                                                  MOLECULAR DYNAMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                #10585 encoded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SYSGKAADVWSLGV 249
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                                                                                                                                                                                                                                                                                                     Hanzel DK,
                                         138 AA;
                                                                                                                                                                                                                                                                                                                                                           2000US-0180312.
2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0236559.
2000US-0236553.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                138 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   liver; gene expression; single exon nucleic acid probe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3.9%;
                                                                                                                                                                                                                                                                                                       Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              by human foetal liver single exon probe
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Score 14;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
                                                                                                                                                                                                                                                                                                        Rank
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                                                                                                                                                                                                                                                                                                        DR;
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2.7e-05;
DB 22;
2.7e-05;
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                                                                                                                                                                                                       English.
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Query Match Best Local

Similarity

3.9%;

Length 138;

Search completed: January Job time: 44 secs

15,

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RESULT 15
AAM63978
ID AAM63
XX AAM63
XX OS-NC
XX Humar
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XX Humar
XX Homo
XX W O9-Al
XX W 09-Al
XX O4-Pl
PR 26-M
PR 30-JI
XX O4-Pl
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Best Local S
Matches 14
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26-MAY-2000; 2000US-0207456.
30-JUN-2000; 2000US-0608408.
03-AUG-2000; 2000US-0632366.
21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0236599.
04-OCT-2000; 2000GB-0024263.
                                                                                                                                                                                                                                  probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is a protein encoded by one o the probes of the invention.
                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; brain expressed exon; microarray; Alzheimer's disea
                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 4; SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-483446/52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09-AUG-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-JAN-2001; 2001WO-US00667.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200157275-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAM63978;
                                                                                                                                                                                                                                                                                                                                                                                     The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      epilepsy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAM63978 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SG,
                                                 236
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  41
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULAR DYNAMICS INC
                                                                                                                     Similarity
                                  SYSGKAADVWSLGV
SYSGKAADVWSLGV 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SYSGKAADVWSLGV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hanzel DK,
                                                                                                                                                                                          138
                                                                                            3.9%; S
llarity 100.0%;
Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                     invention provides a number of single exon nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nucleic acid probes for analyzing gene expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                     ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                36083; 650pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     single
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                                               249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ت
4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               exon; gene expression analysis;
disease; multiple sclerosis; so
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   249
                                                                                            Score 14; DB; Pred. No. 2. 0; Mismatches
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Listing first 45 summaries
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                                                                                                                   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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seq length: 2000000000
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BX325345
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RESULT 1
BG748142
LOCUS
LOCUS
DEFINITION
602705453F1 NIH_MGC_43 Homo sapiens cDNA clone IMAGE:4842324 5',
ACCESSION
RAMA sequence.
BG748142
VERSION
BG748142
VERSION
BG748142.1 GI:14058795
SURCE
SOURCE
ORGANISM
Homo sapiens (human)
ORGANISM
EMARYOLA; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
REFERENCE
1 (bases 1 to 863)
NH-MGC http://mgc.nci.nih.gov/.
NAIJONAL Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT
Email: cgapbs -remail.nih.gov/
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genemics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1676 row: i column: 13
High quality sequence stop: 833.

ALIGNMENTS

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GCGTGCCCAGCCTACGTGGGACCTGAGATACTCAGCTCACGGGCCTCATACTCGGGCAAG
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                                                                                  GAGAACCTGGAGGACTCCTGCGTGCTGACTGGGCCAGATGATTCCCCTGTGGGACAAGCAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="normal pigmented retinal epithelium"
/lab_host="DH108 (phage-resistant)"
/clone_lib="NIH_MGC_43"
/clone_Tib="NIH_MGC_43"
/note="Torgan: eye; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRIXhoI sites using the following 5; adaptor: GCCAGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library. | "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /mol_type= "....9606"
/db_xref="taxon:9606"
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Pred. No. 4.5e-159;
0; Mismatches 11;
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Best Local Similarity 97.5
Matches 866; Conservative
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAMM1323 row: m column: 11
High quality sequence stop: 640.
Location/Qualifiers
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Tissue Procurement: DCTD/DTP/Gazdar
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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AGENCOURT_7570945 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:6058546
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BQ217691
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CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can found through the I.M.A.G.B. Consortium/LLNL at: http://imagge.llnl.gov plate: LLAM13327 row: f column: 02
                                                                       Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP/Gazdar
                                                                                                                                                                                                     BQ216198 873 bp
AGENCOURT 7574831 NIH_MGC_68 Homo
5', mENA Sequence.
BQ216198
BQ216198.1 GI:20397598
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Eukaryota, Metazoa, Chordata, Craniata, V
Mammalia, Eutheria, Primates, Catarrhini,
1 (bases 1 to 873)
11 (bases 1 to 873)
11 H-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished
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/clone_lib="NIH MGC_68"
/clone_Step": lung; Vector: pCNV-SPORT6; Site_1: NotI;
/note="Organ: lung; Vector: pCNV-SPORT6; Site_1: NotI;
/ste_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.8 kb. Library constructed by Life
Technologies. "
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6059905"
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419

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JOURNAL
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Best Local Similarity
Matches 821; Conserv
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Pull-length cDNA libraries and normalization
Unpublished
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cgi-bin/cluster.cgi?seq=CSOALOO4DCO2QP1&cluster=10000.f.
reng Liang Email: fliang@lifetech.com URL:
http://fullength.invitrogen.com/ InvitroGen Corporation
Faraday Avenue Genoscope sequence ID: CSOALOO4DCO2QP1.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 10000.f
more information about this cluster, see
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BX325345 Homo sapiens B
Homo sapiens cDNA clone
BX325345
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Eukaryota; Metazoa;
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                                GCGGGCCTACCGGGCCCTGCACTGCCCCTACAGGCACTGAGTATACCTGCAAGGTGTACCC
                                                                                                                                                       GCCCAGACTGCCCCCCTGCCTGTTGCCCCCTGAGCCCACCTACTGCTCCAGATCGTGCAAC
                                                                                                                                                                                                                          TTGAGATGACAACTTAGATACCGAGCGTCCCGTCCAGAAACGAGCTCGAAGTGGGCCCCA
                                                                                                                                                                                                                                                           TTG-GATGACAACTTAGATACCGAGCGTCCCGTCCAGAAAACGAGCTCGAAGTGGGCCCCA 119
                                                                                                                                                                                                                                                                                                                                   ATGCGAGCCACCCCTCTGGCTGCTCCTGCGGGTTCCCTGTCCAGGAAGAAGCGGTTGGAG
                                                                                                     TGCTGTGGCCACTGCCTCCCGTCTTGGGCCCTATGTCCTCCTGGAGCCCGAGGAGGGCGG
                                                                                                                                                                                                                                                                                                   ATGCGAGCCACCCCTCTGGCTGCTCCTGCGGGTTCCCTGTCCAGGAAGAAGCGGTTGGAG
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                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="18t strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR v sites of the pCMVSPORT 6 vector. Library was normalized a 313 c 282 g 176 t 11 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25 - NORMALIZED"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="mRNA"
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/db_xref="taxon:9606"
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/clone="B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED"
/cell_type="B CELLS (LINE"
/cell_line="RAMOS CELL LINE"
/clone_lib="Homo Bapiens B CELLS (RAMOS CELL LINE) COT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organiem="Homo sapiene"
/mol_type="mRNA"
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Pred. No. 1.2e:
10; Mismatches
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CELLS (RAMOS CELL LINE) COT 25-NORMALIZED
CSODL004YF04 5-PRIME, mRNA sequence.
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. No. 1.2e-156;
ismatches 7;
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                                                                                                                            Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologiss, a division of
Invitrogen. This sequence belongs to sequence cluster 10000.f
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seqecSoDG007AD020P1&cluster=10000.f. Conta
Feng Liang Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com/ InVitroden Corporation 1600
Faraday Avenue Genoscope sequence ID: CSODG007AD020P1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BX421477 Homo sapiens B CELLS (RAMOS CELL clone CSODG007YG03 5-PRIME, mRNA sequence.

BX421477
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1 (bases 1 to 902)
Li W.B., Gruber, C., Jessee, J. and Polayes, D.
Pull-length CDNA libraries and normalization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                       Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                              Bukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Butheria; Primates; Catarrhini; Hominidae;
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/clome="CSODGOOTYGO3"
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                                                                                                         Location/Qualifiers
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       CBLL LINB) "
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839 885 779 825 719 765 659 705 599 645 539 585 479 526

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Matches 81
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/clone_lib="Homo saplens B CELLS (RAMOS CELL LINE)"
/clone_lib="Homo saplens B CELLS (RAMOS CELL LINE)"
/note="Vector: pCMVSPORT 6; lst strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned i
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."

4 others
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Pred. No. 1.4e-155;
2; Mismatches 1;
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CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLN
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information
found through the I.M.A.G.E. Consortium/LINL at:
http://image.llnl.gov
Plate: LLCM2355 row: 1 column: 22
High quality sequence start: 13
High quality sequence stop: 731.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Robert Strausberg,
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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AGENCOURT 7861060 NIH_MGC_64 Homo
5', mRNA Bequence.
BUS00619
BUS00619.1 GI:22801804
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NIH-MGC http://mgc.nci.nih.gov.
National Institutes of Health,
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                             CACAAGCATGTGGCTCGGCCCACTGAGGTCCTGGCTGGTACCCAGCTCCTCTACGCCTTT
                  TTCACTCGGACCCATGGGGACATGCACAGCCTGGTGCGAAGCCGCCACCGTATCCCCTGAG
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/clone_lste_NIH_MGC_64"
/note="Vector: pOTB7a, Site_1: CeuI; Site_2: SceI; This
/note="Vector: pOTB7a, Site_1: CeuI; Site_2: SceI; This
library is a size selection of NIH_MGC_35, from 3.0-4.5
b. Size selection done at the NatTonal Institute of
Mental Health, NIH. Note: this is a NIH_MGC Library."
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/db_xref="taxon:9606"
/clone="IMAGE:6109605"
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95.2%;
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Pred. No. 1.9e-154;
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sapiens cDNA clone IMAGE:6109605
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                                                                                                                               Unpublished
On Feb 15, 2001 this sequence version replaced gi:12899595.
Contact: Genoscope
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: sequencecope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologien, a division of
Invitrogen. This sequence belongs to sequence cluster 10000.
more information about this cluster, see
http://www.genoscope.cns.fr/
                                                                       cgi-bin/cluster.cgi?seq=CSODK005AB03QP1&cluster=10000.f. Feng Liang Email: fliang@lifetech.com UTL: http://fulllength.invitrogen.com/ InVitroGen Corporation Faraday Avenue Genoscope sequence ID: CSODK005AB03QP1. Location/Qualifiers
                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Butheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1201)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization
                                                                                                                                                                                                                                                                                                                                      AL556690 Homo Bapiens HELA CELLS COT 25-NORMALIZED CDNA CLone CSODKOO5YCO5 5-PRIME, mRNA Bequence. AL556690 GI:31278491
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/organism="Homo sapiens"
/mol_type="mRNA"
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/clone="CSODK005YC05"
/cell_type="HELA CELLS COT
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h 71.7%;
Similarity 96.0%;
93; Conservative 1
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                      TTCCAGGACTCGGAGCCTGTCCTGCTCTTCGGCAAGATCCGCCGCG
                                                                                                                    GCGTGCCCAGCCTACGTGGGACCTGAGATACTCAGCTCACGGGCCTCATACTCGGGCAAG
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/clone_lib="Homo sapiens HELA CELLS COT 25-NORMALIZED"
/note="Ist strand cDNA was primed with a NotI-oligo(dT)
/note="Ist strand cDNA was primed double-strand cDNA was
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR v
sites of the pCMVSPORT 6 vector. Library was normalized."
a 366 c 336 g 232 t 62 others
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Pred. No. 2.7e-
15; Mismatches
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1 (bases 1 to 948)

Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

Pull-length cDNA libraries and normalization

Unpublished

Contact: Genoscope
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cgi-bin/cluster.cgi?seq=CSDG007CC03QP1&cluster=10000.f. Contact
Peng Liang Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Paraday Avenue Genoscope sequence ID: CS0DG007CC03QP1.
Location/Qualifiers
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BP 191 91006 EVRY cedex - France
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 10000.f For
more information about this cluster, see
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  GCTCGGCCCACTGAGGTCCTGGCTGGTACCCAGCTCCTACGCCTTTTTCACTCGGACC
                                GCTCGGCCACTGAGGTCCTGGCTGGTACCCAGCTCCTACGCCTTTTTCACTCGGACC
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ilarity 99.4%;
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/cell_line="RAMOS CELL LINE"
/clone_lib="Homo sapiens B CELLS (RAMOS CELL LINE)"
/note="Vector: pCMVSPORT 6; lst strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned i the Not I and ECORV sites of the pCMVSPORT 6 vector. Library was not normalized."

s others
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODG007YP05"
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Pred. No. 6e-150;
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Tissue Procurement: DCTD/DTP/Gazdar
Tissue Procurement: DCTD/DTP/Gazdar
CDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.B. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM13324 row: o column: 19
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:9606"
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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NIH_MGC_64
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Pred. No. 8.7e-148;
O; Mismatches 8;
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: NIMH/LOG
CDNA Library Preparation: NimH/LOG
CDNA Library Preparation: NimH/LOG
CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.B. Consortium/LLNL at: p
http://image.llnl.gov
Plate: LLCM2354 row: c column: 04
High quality sequence stop: 682.
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NIH-MGC http://mgc.nci.nih.gov/
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                                                    GGTCTGGTCCTGCGTGATCTCAAGCTGTGTCGCTTTTGTCTTCGCTGACCGTGAGAGGAAG
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Pred. No. 2.5e-147;
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http://image.lnl.gov
Plate: LLAM11276 row: m column: 10
High quality sequence stop: 820.
Location/Qualifiers
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1 (bases 1 to 820)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Robert Strausberg, Ph.D. Email: cgapbe-r@mail.nih.gov Tiesue Procurement: ATCC
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                                                   AGGAAGAAGCGGTTGGAGTTGGATGACAACTTAGATACCGAGCGTCCCGTCCAGAAACGA 102
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/note="Organ: cervix; Vector: pCMV-SPORT6; Site_1: Not Site_2: Sall; Cloned unidirectionally. Primer: Oligo Site_2: Sall; Cloned unidirectionally. Primer: Oligo Average insert size 1.4 kb. Library prepared by Life Technologies."
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization Unpublished
On Feb 13, 2001 this sequence version replaced Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
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929 bp mRNA linear EST
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AL522632.2 GI:31040900
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Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 10000.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSODB009AH02QP1&cluster=10000.f. Contact
Feng Liang Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CSODB009AH02QP1.
Location/Qualifiers
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/clone_Tib="Homo sapiens NEUROBLASTOMA COT 10-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
a 313 c 284 g 169 t 5 others
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODB009Y003"
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Pred. No. 5.4e-144;
1; Mismatches 1;
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Kristi A. Egland, Ira Pastan
CDNA Library Preparation: Invitrogen Corp
cDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 892)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Location/Qualifiers
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                                                                     CTGAGTATACCTGCAAGGTGTACCCCGTCCAGGAAGCCCTGGCCGTGCTGGAGCCCTATG
                                                                                                                                                                                                                                                                                                                                  155
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/note="Vector: pCMV-SPORT6; Site_1: BcoRV; Site_2: Not I;
/note="Vector: pCMV-SPORT6; Site_1: BcoRV; Site_2: Not I;
Subtracted with brain, liver, lung, kidney and muscle.
Directionally cloned. Priming method: oligo-dT. Average
insert size: 1800 bp. Library amplification: 26,000 fold.
Kristi A. Egland, James J. Vincent, Robert Strausberg,
Bungkook Lee & ITa Pastan: Discovery of new breast
cancer genes encoding membrane and secreted proteins.
                                                                                                                                                                                                                                                                                                                                  Manuscript submitted."
309 c 267 g 1
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/mol_type="mRNA"
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/clone="IMAGE:6785470"
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97.5%;
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Pred. No. 3e-143;
0; Mismatches 16;
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ISM Homo Sapiens

Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Bukaryota, Metazoa; Primates; Catarrhini; Hominidae; Homo.

CE 1 (bases 1 to 1126)

RS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

Full-length cDNA libraries and normalization

Unpublished

Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 10000.f For

more information about this cluster, see

http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSDAM009CC08QP1&cluster=10000.f. Contact:
Feng Liang Email: filang@lifetech.com URL:
Feng Liang Email: filang@lifetech.com URL:
Feng Liang Email: filang@lifetech.com URL:
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Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqrefegenoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 10000.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSODKOO8BBO5QP1&Cluster=10000.f. Contact:
cgi-bin/cluster.cgi?seq=CSODKOO8BBO5QP1&Cluster=10000.f.
Feng Liang Email: fliang&lifetech.com URL:
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CSODKOO8BBO5QP1.

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BX363066 Homo Bapiens HELA CELLS
CDNA clone CSODKOOBYC10 5-PRIME,
BX363066
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1. (bases 1 to 944)
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EST.
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                                                                                                         CGGGCCTACCGGGCCCTGCACTGCCCTACAGGCACTGAGT&TACCTGCAAGGTGTACCCC
                                                                                                                                                                                          GCTGTGGCCACTGCCTCCCGTCTTGGGCCCCTATGTCCTCCTGGAGCCCCGAGGAGGGCGNG
                                                                                                                                                                                                                                                       GCTGTGGCCACTGCCTCCCGTCTTGGGCCCTATGTCCTCGTGGAGCCCGAGGAGGGCGGG 240
GTCCAGGAAGCCCTGGCCGTGCTGGAGCCCTACGCGCGGCTGCCCCCGCACAAGCATGTG
                                                                CGGGCCTACCGGGCCCTGCACTGCCCTACAGGCACTGAGTATACCTGCAA-GTGTACCCC
                                                                                                                                                                                                                                                                                                                           CCCAGACTGCCCCCCCTGTTGCCCCCTGAGCCCACCTACTGCTCCAGATCGTGCAACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                         TTGGATGACAACTTAGATACCGAGCGTCCCGTCCAGAAACGAGCTCGAAGTGGGCCCCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone lib="Homo sapiens HELA CELLS COT 25-NORWALIZED"
/note="lst strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and Ecor V
sites of the pCMVSPORT 6 vector. Library was normalized."
a 315 c 296 g 168 t 8 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
|mol type="mRNA"
|/mol type="mRNA"
|/db xref="taxon:9606"
|/db xref="taxon:9606"
|/clne="c50DK008YC10"
|/cell type="HELA CBLLS COT 25-NORMALIZED"
|/cell line="HELA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        66.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 711; DB 13; 1
Pred. No. 5.9e-138;
1; Mismatches 2;
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COT 25-NORMALIZED
mRNA sequence.
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Search completed: January 16, Job time: 2414.84 secs 2004, 16:46:21

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Title:
Perfect score:
Sequence:
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Maximum DB
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Listing first 45 s
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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seq length: 2000000000
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1: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1980.DAT:*
2: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*
3: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1982.DAT:*
4: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1983.DAT:*
5: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1984.DAT:*
6: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1984.DAT:*
6: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1986.DAT:*
7: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1986.DAT:*
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                                                                                                                         | SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1987, DAT: *
| SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1988, DAT: *
| SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1988, DAT: *
| SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1989, DAT: *
| SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1999, DAT: *
| SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1999, DAT: *
| SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1992, DAT: *
| SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1992, DAT: *
| SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1993, DAT: *
| SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1994, DAT: *
| SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1995, DAT: *
| SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1997, DAT: *
| SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1999, DAT: *
| SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1999, DAT: *
| SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2000, DAT: *
| SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2001A, DAT: *
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Regult	Score	Query Match	Query Match Length DB	80	ID	Description
1	1070.8	99.7	1077	22	22 AAS06709	Polynucleotide seq
N	1069.2	99.6	2059	22	AAI59850	Human polynucleoti
w	1069.2	99.6	2092	22	AAI58064	Human polynucleoti
4	1069.2	99.6	2116	22	AAF30480	Human protein phos
_S	1051.6	97.9	1083	24	ABN86479	Human tribbles hom
<u>چ</u>	956.4	89.1	1085	21	AAZ61155	cDNA JJ503-KS enco
}	879.2	81.9	2048	21	AAC77866	Human cancer assoc
ر 8	799.2	74.4	972	22	AAH76218	Human kinase PKIN-
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885	108.2	156	156	156	158	158	158	158	158	158	163.6	165	207.6	220.8	222.2	232.4	233.4	234	236.2	247	251.4	263.2	274.2	282.2	•	•	•	597.2
7.9	7.9		14.5		•	•		14.7	٠	14.7	15.2	15.4	19.3	•			21.7		•	23.0	23.4		25.5	26.3	9	39.7	55.6	5
1302 1302 1302	6988 1302	417	417	417	25772	562	562	562	562	562	7282	498	1943	562	621	818	942	675	690	3324	3280	1909	3319	396	534	2562	1076	1076
220	23	2 2 2	222	22	2 22	24	23 1) N	22	22	22	24	22	21	25	25	25	24	24	24	25	22	24	22	23	16	24	24
AAX79647 AAX39660 ABA03938	ABL29124 ABL29124 AAT38285	ABS48709 ABS22668	AAK49052 AAI54879	AAK22879	AAK81332	ABS10267	ABS35823	AAK36130	AAK10231	ABA61922	AAK86318	ABK63084	AAS45223	AAC78131	ACC45126	ACC45125	ABX74428	ABK83550	ABT09024	AAS94913	ABX63269	AAS45035	ABN86478	AAS37461	AAS68600	AAQ89817	ABL39762	ABL39747
Human LKB1 coding Renal cancer assoc Human STK11 coding	Drosophila melanog Drosophila melanog Protein kinase cDN	Human liver single Human genome-deriv	Probe #23565 used	Human brain expres	-	-	Human liver single		-	Human foetal liver	Human immune/haema	Rat sequence diffe	cDNA encoding nove	cance	CBPW	C8FW	CDNA	Human cDNA differe			Human cDNA #269 di	cDNA encoding nove	Human tribbles hom	Novel human diagno	DNA encoding novel	~	Human NS cDNA eequ	Human NS cDNA eequ

ALIGNMENTS

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RESULT 1
AASO709
ID AASO709
XX AASO
XX AASO
XX Poly
T12-S
XX Huma
KW meta
KW repr
XX repr
XX Homo
XX VO20
XX 1-M
XX 1-M
XX 22-N
XX 22-N
XX 24-N
XX SHOW
PF 22-N
XX Y 1-M
XX Y 
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Polynucleotide sequence encoding human protein kinase

Human; protein kinase; PTK; STK; cancer; cardiovascular disease; metabolic disorder; immune related disease; neurological disorder; neurodegenerative disorder; inflammatory disorder; infectious disease; reproductive disorder; gene therapy; ss.

Homo sapiens.

WO200138503-A2

31-MAY-2001.

22-NOV-2000, 2000WO-US32085

24-NOV-1999; 99US-0167482

(SUGB-) SUGEN INC.

Plowman GD, Flanagan P, Whyte D, Clary D; Manning G, Sudarsanam S, Martinez R;

WPI, 2001-343950/36

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CC AASO6701-AASO6757 encode for novel human protein kinases #1-57. The CC novel protein kinases have been identified as members of the tyrosine CC or serine/threonine kinase (PTK and STR) families. The polynuclectides CC encoding protein kinases and the polypeptides may be used in the CC prevention, diagnosis and treatment of diseases associated with CC inappropriate kinase expression. For example, they may be used to treat CC cancers (especially cancers of haematopoietic origin), cardiovascular CC disease (e.g. atheroselerosis), metabolic disorders (e.g. diabetes), CC immune related diseases (e.g. rheumatorid arthritis), neurological CC disorders (e.g. schizophrenia), neurodegenerative disorders (e.g. CG Parkinson's disease), inflammatory disorders (e.g. ashma), infectious CC disease (e.g. HIV) and reproductive disorders (e.g. ashma), infectious CC disease (e.g. bolynuclectides encoding protein kinases may be used as antigens in the production CC of antibodies against the protein kinases and in assays to identify CC modulators of protein kinase expression and activity.
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Best Lucal Sim
Matches 1072;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1077
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                                                                                                                                                                                                                           CATGGGGACATGCACAGCCTGGTGCGAAGCCGCCACCGTATCCCTGAGCCTGAGGCTGCC
GAGAACCTGGAGGACTCCTGCGTGCTGACTGGGCCAGATGATTCCCTGTGGGACAAGCAC
                                           CGTGATCTCAAGCTGTGTCGCTTTGTCTTCGCTGACCGTGAGAGGAAGAAGCTGGTGCTG
                                                                      CGTGATCTCAAGCTGTGTCGCTTTGTCTTCGCTGACCGTGAGAGGAAGAAGCTGGTGCTG
                                                                                                                                    GTGCTCTTCCGCCAGATGGCCACCGCCCTGGCGCACTGTCACCAGCACGGTCTGGTCCTG
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Pred. No. 6.1e-231;
0, Mismatches 2;
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25-APR-2000; 2000US-0552317.

09-JUL-2000; 2000US-0598042.

19-JUL-2000; 2000US-0620312.

03-AUG-2000; 2000US-0653450.

14-SEP-2000; 2000US-0662191.

19-OCT-2000; 2000US-0693036.

29-NOV-2000; 2000US-0727344.
                                     Tang
Wang
Zhao
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29-NOV-2000;
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The invention relates to human nucleic acids (AAI57798-AAI61369) and CC the encoded polypeptides (AAM32642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polypuclectides are useful CC in gene therapy. A composition containing a polypeptide or polynuclectide cC of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and CC localised neuropathies and central nervous system diseases, such as CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the CC utilisation of the activities such as: Immune system suppression, CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic assays for receptor activity, cancer diagnosis and therapy, drug screening, CC assays for receptor activity, arthritis and inflammation, leukaemias and CC ute: The sequence data for this patent did not form part of the printed of the printed content of the content of the printed content of t
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  Claim
                                     Novel human protein phosphatase and kinase proteins for diagnosis, treatment and prevention of gastrointestinal, immune system, neurological and cell proliferative disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein phosphatase and kinase protein; PPHKP-5; human; gastrointestinal disorder; immune system disorder; cancer; neurological disorder; cell proliferative disorder; cancer;
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P-PSDB; AAB20326.
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                                                                                                    Novel isolated human tribbles homologue-1 polypeptide for inhibiting AP-1-mediated inflammatory signal in a cell, and activating ERK-mediated signal e.g. AP-1-mediated gene activation signal in a co
                                                                                                                                                                                                                                                                                                                                                                                                       08-JAN-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; tribbles; htrb-1; stress kinase inhibitor protein; SKIP-1; AP-1; antifrheumatic; antiathritic; antidiabetic; antipsoriatic; osteopathic; opthalamological; cardiant; cytostatic; haemostatic; immunosuppressive; antiinflammatory; estrogen receptor; fibroblast growth factor; FGP; tumour necrosis factor; TNP; gene; htrb-3; ds.
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CC also known as stress kinase inhibitor protein (SKIP-1)) polypeptide. The CC htrb polypeptide is useful for inhibiting an AP-1 mediated inflammatory CC signal in a cell. The polypeptide employed in the method is preferably CC htrb-1, htrb-1 C, htrb-1 N C, htrb-3, htrb-3 N cr If is also useful for providing htrb agonist activity for CC activating an ERK-mediated signal e.g. AP-1-mediated gene activation cC signal, an estrogen receptor-mediated gene activation signal, an cell. Htrb modulators are useful for modulating AP-1 mediated inflammatory signal in a cell such as tumor necrosis factor (TNP) CC induced inflammatory signal, or an interleukin induced inflammatory signal, or an interleukin induced inflammatory compounds e.g. for treating and/or preventing diseases caused by abnormal htrb activity, such as rheumatoid arthritis, disbetes, psoriasis, osteoporosis, diabetic retinopathy, myocardial infarction contents and sorteoporosis, diabetic are useful for antagential infarction and cancers. The htrb therapeutics are useful for antagential infarction contents white matter damage and subsequent cerebral palsy, and inflammation or autoimmune disorders. The present sequence represents a DNA encoding the htrb-3 polypeptide.
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Best Local Similarity
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The present sequence encodes a partial polypoptide which has k activity. The kinase polymucleotides can be used to express the polypoptides, and as probes to identify nucleic acids encoding polypoptides, and as probes to identify nucleic acids encoding proteins having kinase activity. The kinase polypoptides and
                                       Claim 1;
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11-SEP-1998;
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fragmented polypeptides are used as molecular weight and isoelectric focusing markers, and as controls for peptide fragmentation. They also have a number of therapeutic uses as kinases play a central role in cellular signal transduction. The polypeptides could also be used to identify binding partner proteins. The polypeptides can also be used as a reagent to identify any proteins that the polypeptide regulates, and proteins with which it might interact. The polypeptides may also be used for preparation of antibodies. The antibodies can be used in assays to detect the presence of the protein, and to purify the protein immunoaffinity chromatography.

Sequence 1085 BP; 164 A; 389 C; 338 G; 194 T; 0 other;

ភភភភភភភភភភភភភន្ត Query Match Best Local Sim Matches 957; Similarity Conservative 89.1**%**; 0 Score Pred. Mismatches 956.4; No. 2.9 .9e-205; зев 1; BB 21; Indels Length 0,

ફ 밁 ક 8 ş 밁 ક ક 밁 밁 ş 밁 र् 밁 ð 밁 밁 र् 밁 ş 밁 ঠ 밁 र् 밁 र् 806 781 848 788 661 109 668 541 809 548 721 728 481 GCGTGCCCAGCCTACGTGGGACCTGAGATACTCAGCTCACGGGCCTCATACTCGGGCAAG GAGAACCTGGAGGACTCCTGCGTGCTGACTGGGCCAGATGATTCCCTGTGGGACAAGCAC CGTGATCTCAAGCTGTGTCGCTTTGTCTTCGCTGACCGTGAGAGGAAGAAGCTGGTGCTG TTCCAGGACTCGGAGCCTGTCCTGCTCTTCGGCAAGATCCGCCGCGGGGCCTACGCCTTG GCGTGCCCAGCCTACGTGGGACCTGAGATACTCAGCTCACGGGCCTCATACTCGGGCAAG GAGAACCTGGAGGACTCCTGCGTGCTGACTGGGCCAGATGATTCCCTGTGGGACAAGCAC GTGCTCTTCCGCCAGATGGCCACCGCCCTGGCGCACTGTCACCAGCACGGTCTGGTCCTG GTGCTCTTCCGCCAGATGGCCACCGCCCTGGCGCACTGTCACCAGCACGGTCTGGTCCTG 840 967 907 847 787 660 727 600 667 540 607

> ક 밁 밁 ફ 1028 901 896 841 GCTGAACGGCTCACAGGCACAGGCATCCTCCTGCACCCCTGGCTGCGACAGGACCCGA 1085 GCTGAACGGCTCACAGCCACAGGCATCCTCCTGCACCCCTGGCTGCGACAGGACCCGA 958 2048 ₽P

AAC77866 standard; CDNA;

08-FEB-2001

Human cancer associated gene веquence SEQ B NO:260.

RESULT 7
AAC77866
ID XX
AAC77866
XX
AAC77866
AAC77866
AAC77866
AAC7786
AAC786
A diagnosis; cytostatic; proliferative; vulnerary; immunomodulator; antidiabetic; antiasthmatic; antirheumatic; antiarthritic; antiviral; antiinflammatory; antiprovid; antiartergic; antibacterial; cardiant; dermatological; neuroprotective; thrombolytic; coagulant; nootropic; vasotropic, antipsoriatic; antianglegalic; gene therapy; inflammation; immune disorder; antipsoriatic; antianglegalic; gene therapy; inflammation; immune disorder; antipsorietic cell disorder; autoimmune disorder; altergic reaction; graft versus host disease; organ rejection; haemospatatic; thrombolytic; cardiovascular disorder; infection; neurological disease; Human; cancer associated gene; screening; ss. cancer antigen; detection; cancer;

Homo sapiens.

WO200055350-A1

08-MAR-2000; 2000WO-US05882

12-MAR-1999; (HUMA-) HUMAN GENOME 99US-0124270

S

2000-587533/55 DB; AAB43657.

Claim 1, Page 2352pp; English.

CC AAC77607 to AAC78448 encode the human cancer associated proteins given CC in AAB43398 to AAB4239. The proteins can have activities based on the CC tissues and cells the genes are expressed in. Example of activities CC include: cytostatic, proliferative, vulnerary; immunomodulator; cinclude: cytostatic, proliferative; vulnerary; immunomodulator; cc antidiabetic; antissthmatic; antishlergic; antibacterial; antiviral; cc antiinflammatory; antithyroid; antiallergic; antibacterial; antiviral; cc antiinflammatory; antipsoriatic; and antianglogenic. The cc mootropic; vasocropic; antipsoriatic and antianglogenic. The cc mootropic; vasocropic; antibodies can be used for preventing, treating or cc meliorating medical conditions and diagnosing pathological conditions. CC polynucleotides, polypeptides antibodies, agonists and antagonists from cc the present invention may be used to treat immune disorders by activating cr immune cells, to treat disorders, differentiation or mobilisation of cc inflammation, cancers, cardiovascular disorders, neurological disease and cr rejection, modulate haemostatic or thrombolytic activity, modulate inflammation, cancers, cardiovascular disorders, neurological disease and cc agonists and antagonists may be also be used in drug screens. AAC78449 to AAC78457 and AAB44240 represent sequences used in the exemplification of the present invention of the present sequences used in the exemplification of the present sequences used in the p

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                          GCTGAACGGCTCACAGCCACAGGCATCCTCCTGCACCCCTGGCTGCGACAGGACCCGATG
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                                                                                                                                   GCGTGCCCAGCCTACGTGGGACCTGAGATACTCAGCTCAMGGGCCTCATACTCGGGCAAG
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92.6%;
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Hafalia A, Shih LL,
Zingler KA, Lu DAM,
Nguyen DB, Lal P, Wa
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02-MAR-2000; 2000US-0186559.

09-MAR-2000; 2000US-0188606.

17-MAR-2000; 2000US-0189998.

30-MAR-2000; 2000US-0193851.
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P-PSDB; AAB85791.
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Tribouley CM, Yao MG,
Bandman O, Policky JL,
Walsh RT;
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Burrill JD,
Griffin JA,
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/D, Marcus GA;
·TA, Thornton ↑
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growth isolated human kinase polypeptides useful in the diagnosis, treatment and prevention of cancer, immune disorders and disorders affecting and development

Claim 5; Page 125; 126pp; English.

The invention provides human kinases (PKIN) and polynucleotides encoding PKIN. The PKIN polypeptides can be expressed using standard recombinant methodology. The PKIN polypeptides, polynucleotides, modulators and specific antibodies are useful in the diagnosis, treatment and prevention of cancer, immune disorders, disorders affecting growth and development, atherosclerosis, and other cardiovascular diseases, and lipid disorders and in the assessment of the effects of exogenous compounds on the expression of nucleic acid sequences of human kinases. The present sequence represents a cDNA encoding a human PKIN-10 polypeptide.

Sequence 972 BP; 167 A; 329 C; 294 G; 182 T; 0 other;

ફ Query Match Best Local Similarity Matches 941; Conserv ATGCGAGCCACCCCTCTGGCTGCTCCTGCGGGTTCCCTGTCCAGGAAGAAGCGGTTGGAG Conservative 74.4%; 87.6%; <u>.</u> Score 799.2; DB 22; Pred. No. 5.5e-170; 0; Mismatches 28; Indels Length 105; Gaps 60

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18-JUL-2000; 2000IL-0137345. 15-DEC-2000; 2000IL-0140354.

LTD.

Mintz L, Freilich S,

WPI; 2002-155037/20 ABB06093.

One hundred and twenty eight novel nucleic acid sequences, useful treating and diagnosing e.g. cancer, asthma and Alzheimer's -

Claim 1, Page 107; 290pp; English.

CC ABL39691 to ABL39818 represent novel human nucleic acid sequences CC encoding the proteins given in ABB06037 to ABB06164. The novel sequences CC (NS) can have cytostatic, osteopathic, synaecological, neuroprotective, CC vasotropic, antiarthritic, antipporiatic, ophthalmological, virucide, CC vasotropic, antiarteriosclerotic, antinfermility, cardiovascular, antifibrinolytic, hypotension, antiasthmatic, cardiant, CC annorectic, muscular, anti-HIV, antiinfertility, cardiovascular, cardiant, CC antideogram, anticonvulsant, antidabetic, tranquilliser, antiulcer, CC antideopressant, gastrointestinal, aeuroleptic, cerebroprotective, antideopressant, gastrointestinal, aeuroleptic, cerebroprotective, CC noctropic and contraceptive activities. The NS can be used in vaccines, CC gene therapy and antisanse therapy, Nucleic acids, expression vectors and CC diagnosing e.g. cancer, osteoporosis, endometriosis, degenerative and CC diagnosing e.g. cancer, osteoporosis, endometriosis, degenerative, contracter, cateronia, multiple sclerosis, inflammation, skin disorders, CC glaucoma, obesity, muscular dystrophy, AIDS, infertility, cardiovascular CC disease, coagulation disease, isohaemia, hypertension, asthma, immune CC disease, coagulation disease, isohaemia, hypertension, asthma, immune CC disease, epilepsy, angina, neurodegeneration, diabetes, anxiety, CC Alzheimer's disease and as a contraceptive.

Sequence 1076 BP; 172 A; 352 C; 346 G; 194 T, 12

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Query Match Best Local S Matches 622 Similarity 55.6%; 98.1%; Score 597.2; Pred. No. 1.2 ed. No. 1.2e-124; Mismatches 6; DB. 24; Indele Length 1076; ų. Gaps 2

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CC ABL39691 to ABL39818 represent novel human nucleic acid sequences CC encoding the proteins given in ABB06037 to ABB06144. The novel sequences CC (NS) can have cytostatic, osteopathic, gynaecological, neuroprotective, cantirheumatic, antiarthritic, antisportatic, ophthalmological, virucide, vasotropic, antiarteriosclerotic, antisportatic, ophthalmological, virucide, canorectic, muscular, anti-HTV, antiinferrility, cardiovascular, cardiant, anticoagulant, antifibrinolytic, hypotension, antiasthmatic, cardiant, cimmunomodulator, anticonvulsant, antidabetic, tranquilliser, antiulcer, cimmunomodulator, anticonvulsant, antidabetic, tranquilliser, antiulcer, cantidepressant, gastrointestinal, acuroleptic, cerebroprotective, antidepressant, gastrointestinal, acuroleptic, cerebroprotective, concerpic and contraceptive activities. The NS can be used in vaccines, complete and antisense therapy. Nucleic acids, expression vectors and cantibodies from the present invention can be used for treating and contraceptive activities, endometriosis, degenerative diseases, dystonia, multiple sclerosis, rheumatoid arthritis, psoriasis, contenses, obesity, muscular dystrophy, AIDS, infertility, cardiovascular disease, epilepsy, angina, neurodegeneration, bein disease, anthere, contenses, schizophrenia, viral disease, gastric ulcers, anxiety, candiovascular disease, disease and as a contraceptive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                One hundred and twenty eight novel nucleic acid sequences, useful treating and diagnosing e.g. cancer, asthma and Alzheimer's -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim
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15-DBC-2000; 2000IL-0140354.
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Sequence 1076 BP; 172 A; 352 C; 346 G; 194 T; 12 other;

Local Similarity

55.6%; 98.1%;

24;

Length

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 Query Match
Best Local
                                                                          The sequence is that of the DNA encoding AUP1 (AU-rich element RNA-binding factor-1). AUP1 can be used to treat humans with low levels of the AUP1 gene, so limiting the expression of a proto-oncogene (pref. c-myc, c-myb or c-fos) which when over expressed, leads to
                            Sequence
                                                                                                                                            AUF1 polypeptide and DNA encoding it - limits the expression proto-oncogene that, when over expressed, leads to cancer.
                                                                                                                          Claim 3, Pig
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27-NOV-1995
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                                              See also AAQ89818-20.
(Updated on 25-MAR-2003 to correct PN
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DB; AAR74201.
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39.7%;
93.8%;
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New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                            31-MAR-2000;
23-AUG-2000;
                                                                                                                                                                                                                                                                                                                              30-MAR-2001; 2001WO-US08631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; chromosome mapping; gene mapping; gene therapy; food supplement; medical imaging; diagnostic; genetic of
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DB; ABG04413.
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Best Local S
Matches 290
                    09-MAR-2001; 2001WO-US07787.
                                                                                                                                                                                                                                     Novel
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                                                               13-SEP-2001
                                                                                                                                                                                          Human; cancer; breast;
                                                                                                                                                                                                                                                                              17-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                  AAS37461 standard, cDNA; 396 BP
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                                                                                                                                                                                                                                   diagnostic and therapeutic gene #519.
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                                                                                                                                                                                                                                                                              entry)
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99.7%;
                                                                                                                                                                                       lung; colon; prostate; cytostatic; diagnostic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 289.4; |
Pred. No. 1.3e
0; Mismatches
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Best Local S
Matches 287
                                                Human; tribbles; htrb-1; stress kinase inhibitor protein; SKIP-1; AP-1; antifibumatic; antiathritic; antidabetic; antipsoriatic; osteopathic; opthalamological; cardiant; cytostatic; haemostatic; immunosuppressive; antiinflammatory; estrogen receptor; fibroblast growth factor, PGP; tumour necrosis factor; TNP; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to new polynucleotides and polypeptides, useful for diagnosis and treatment of breast, lung and colon cancer. The sequences can be used in detecting differentially expressed genes correlated with a cancerous state of a mammalian cell, comprising detecting at least one differentially expressed gene product in a test sample derived from a cell suspected of being cancerous. They can also be used to inhibit tumour growth by modulating expression of a gene product. AAS36943-AAS39338 represent novel human diagnostic and therapeutic coding sequences of the invention.
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Drmanac R, Cr
Leshkowitz D,
                                                                                                                                         Human tribbles
                                                                                                                                                                      21-OCT-2002
                                                                                                                                                                                                  ABN86478;
                                                                                                                                                                                                                               ABN86478 standard; cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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Reinhard C,
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(HYSB-)
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HYSEQ INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Page 727; 1193pp; English
                                                                                                                                                                                                                                                                                                     CGGTCCTACCAGGCCCTGCACTGCCCTACAGGCACTTGAGATACCTGCAAGGTGT
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Crkvenjakov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                     (first entry)
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                                                                                                                                     homologue-1 (htrb-1) polypeptide encoding cDNA
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Garcia V,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 282.2; |
Pred. No. 5e-5
0; Mismatches
                                                                                                                                                                                                                               ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Jones WL,
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Pot D, Kassam A, Lamson
, Drmanac S, Labat I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5e-54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  for diagnosis
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CC also known as stress kinase inhibitor protein (SKIP-II) polypoptide. The CC htrb polypoptide is useful for inhibiting an AP-1 mediated inflammatory cc signal in a cell. The polypoptide employed in the method is preferably cc htrb-1, htrb-1 N htrb-1 C, htrb-1 N C, htrb-3, htrb-3 N htrb-3 C, or cc htrb-3, ntr is also useful for providing htrb agonist activity for c activating an ERK-mediated signal e.g. AP-1-mediated gene activation cc signal, an estrogen receptor-mediated gene activation signal, an cell. Htrb modulators are useful for modulating AP-1 mediated signal, or a cell. Htrb modulators are useful for modulating AP-1 mediated cinflammatory signal in a cell such as tumor necrosis factor (TNP) crimduced inflammatory signal, or an interleukin induced inflammatory compounds are useful in screening assays, predictive medicine and in therapeutics or prophylactics. The htrb proteins are useful for screening compounds e.g. for treating and/or preventing diseases caused by abhormal htrb activity, such as rheumatoid architits, diabetes, compounds e.g. for treating and/or preventing diseases caused by abhormal htrb activity, such as rheumatoid architits, diabetes, compounds e.g. for treating and/or preventing diseases caused conditions of the caused of the caused of the caused disease are useful for antagonizing conditions a
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P-PSDB; ABB80975.
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/product= "htrb-1"
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Pred. No. 4.6
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RESULT 15 AAS45035 ID AAS45

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AAS45035 standard; cDNA; 1909

18-DEC-2001 (first entry)

cDNA encoding novel human secretory protein, Seq ij ĕ

Human; secreted protein; arthritis; Crohn's disease; sepsis; shock; ischaemia-reperfusion injury; haematopoiesis; cancer; neuropathy; transgenic animal; Alzheimer's disease; Parkinson's disease; burn; amyotrophic lateral sclerosis; platelet disorder; thrombocytopenia; ulcer; osteoporosis; bone degenerative disorder; periodontal disease; gut protection; lung; liver fibrosis; immune deficiency; infection; severe combined immunodeficiency; SCID; autoimmune disorder; allergy; multiple sclerosis; rheumatoid arthritis; diabetes mellitus; asthma; fertility; analgesic; pain,

13-SEP-2001.

05-MAR-2001; 2001WO-US04942.

07-MAR-2000; 19-MAY-2000; 17-JUN-2000; 14-JUL-2000; 19-SBP-2000; 20-OCT-2000; ; 2000US-0519705. ; 2000US-0574454. ; 2000US-0596193. ; 2000US-0616847. ; 2000US-0665363. ; 2000US-0693267.

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CC prophylaxis or treatment of one or more cancers. (II) is also useful for CC creating transgenic animals useful for studying the in vivo activities of the polypeptide as well as for studying modulators of the polypeptides. (I) induces the proliferation of neural cells and regeneration of nerve CC and brain tissue and is useful for the treatment of central and CC peripheral nervous system diseases and neuropathies, such as Alzheimer's, creativity, regulation of haematopoiesis and is useful for treating myeloid or lymphoid cell disorders, platelet disorders such as thrombocytopenia CC activity, regulation of haematopoiesis and is useful for treating myeloid or lymphoid cell disorders, platelet disorders such as thrombocytopenia CC ulcers, for treating osteoporosis, osteoarthritis, bone degenerative disorders, or periodontal disease. Furthermore, (I) is also useful for cylerission injury in various tissue, various immune deficiencies and constitis, diaberes mellitus, myasthenia gravis, allergic resections, autoimmune disorders e.g. multiple sclerosis, creations, autoimmune disorders e.g. multiple sclerosis, compatitity, metabolism, catabolism, anabolism, storage or elimination of distary fat, lipid, protein, carbohydrate, vitamins, minerals, provides analgesic effects or other pain reducting effects, immunoglobulin like catabone. Ahs44920-Ahs45295 represent novel human secreted protein codding sequences of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 447; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1909 BP; 472 A; 535 C; 435 G; 467 T; 0 other;
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TGGCGCACTGTCACCAGCACGGTCTGGTCCTGCGTGATCTCAAGCTGTGTCGCTTTGTCT
                                                    GCCGGAAGAGGCTGCGGGAAGAGGAAGCCGCCCGGCTCTTCAAGCAGATTGTCTCCGCCG
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                                                                                                                                                                  ANACCAAGGCCTATGTCTTCTTTGAGAAGGACTTTGGGGACATGCACTCCTATGTGCGAA
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Pred. No. 1.2e-49;
0; Mismatches 288
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T, Zhang J, Chen R,
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Search completed: January 16, Job time: 311.409 Becs 2004, 11:33:02

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SUMMARIES

VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS	RESULT 1 AX166518 LOCUS DEFINITION ACCESSION			10 65 11 11 15 15 15 15 15 15 15 15 15 15 15	
AX166518.1 Homo sapid Homo sapid Bukaryota Mammalia; 1 Plowman, G Planagan, B	AX166518 Sequence	236.2 234 222.2 217.8 210.8 165 163.6	4		
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H	atent	9655296			; ₀
63 nordata; Craniata; rimates; Catarrhini ., Manning,G.S., Su .D.S.	ALIGNMENTS 1077 bp DNA WC0138503.	AX525590 HSCBFW HSCC27159 AY247742 AY254200 AX4051315 AF179296	AF2504310 AF205437 HSM003696 BC006800 AF258866 AF247741 AF24544 D87119 AF205438 CFC5FW CFC5FW CFC5FW CFC5FW CFC5FW CFC5FW CFC5FW CFC5FW CFC5FW	10 AP358868 AX364906 AX364921 BC012955 BS103G7 AR274998 BSU02019 BSU02019 AR27432 AC023322 AC0233773 AC133773 AC133773 AX252894 AX2455894	SUMMARIES ID AX166518 BC019363 BC027484 AY247738 AX26945 AX026945 AX572896 AX572896 AX572896 AX573896 AX573896 AX573896 AX573896
Vertebrata, Buteleostomi, , Hominidae, Homo. dareanam,S.S., Martinez,R., kinase-like enzymes	linear PAT 22-JUN-2001	രയമെ	AF250310 Homo sapi AF250377 Homo sapi AL832388 Homo sapi BC006800 Mus muscu AF358866 Mus muscu AF358866 Mus muscu AY247741 Bos tauru BC002637 Homo sapi AY24524 Homo sapi AY265244 Homo sapi AF255438 Rattus no AX281759 Sequence X99144 C. familiari AF338867 Mus muscu BC034338 Mus muscu	mus mus mus mus mus mus mus mus	Description AX16518 Sequence BC019363 Homo sapi BC027484 Homo sapi AY247738 Homo sapi AX099934 Sequence AX026945 Homo sapi AX572896 Sequence AR257311 Homo sapi AX224734 Sequence

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                     TTCCAGGACTCGGAGCCTGTCCTGCTCTTCGGCAAGATCCGCCGCGGGGGCCTACGCCTTG
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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Klausner, R.D., Collins, F.S., Wagner, L., Sheamen, C.M., Schuler, G.D.,

Altschul, S.F., Zeeberg, B., Buctow, K.H., Schaefer, C.P., Bhat, N.K.,

Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Heleh, P.,

Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,

Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,

Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,

Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,

McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,

McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,

McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,

Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,

Villalon, D.K., Muzny, D.M., Sodergren, B.J., Lu, X., Gibbs, R.A.,

Pahey, J., Helton, B., Ketteman, M., Madan, A., Rodrigues, S.,

Pahey, J., Helton, B., Ketteman, M., Madan, A., Rodrigues, S.,

Pahey, J., Helton, B., Ketteman, M., Madan, J.W., Green, B.D.,

Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, B.D.,

Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schwucz, J., Myers, R.M.,

Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,

Schnerch, A., Schein, J.E., Jones, S.J., and Marra, M.A.

Generation and initial analysis of more than 15,000 full-length

human and mouse cDNA sequences

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield, Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin, Letticia Halao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott, Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy,
                                                                                                                                                                                                          CDNA Library Preparation: Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.B. Co. DNA Sequencing by: Genome Sequence Centre, BC Cancer Agency, Vancouver, BC, Canada info@bcgsc.bc.ca
                                                                                                                                                                                                                                                                                                                                                            Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
Submitted (13-DEC-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                    NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 11056039.
                                                                                                                                                                                                                                                                                                                                                                                                            1 ATGCGAGCCACCCCTCTGGCTGCTCCTGCGGGTTCCCTGTCCAGGAAGAAGCGGTTGGAG
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                   CATGGGGACATGCACAGCCTGGTGCGAAGCCGCCACCGTATCCCTGAGCCTGAGGCTGCC
                                                                         GCTCGGCCCACTGAGGTCCTGGCTGGTACCCAGCTCCTACGCCTTTTTCACTCGGACC
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/tranelation="MRATPLARPASLSRKKRLELDDNLDTERPVQKRARSGPQPRLP
/cranelation="MRATPLARPASLSRKKRLELDDNLDTERPVQKRARSGPQPRLP
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VLFRQMATALAHCHQHGLULRDLKLCRFVFADRERKKLVLENLEDSCYLLTGFDDSLMD
KHACPAYVGPBILSSRASYSGKAADDWSLGVALFTMLAGHYPFQDSEPVLLFGKIRRG
AYALPAGLSAPARCLVRCLLREBPAERLTATGILLHPMLRQDPMPLAPTRSHLMBAAQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="chromosome 20 open 
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/note="symonyms: dJ1103G7.3,
/db_xref="LocusID:57761"
108. .1184
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/mol type="maNA"
/mol type="maNA"
/db xref="taxon:9606"
/clone="MGC:854 IMAGE:3528490"
/tlssue type="Muscle, rhabdomyosarcoma"
/clone Ib="NIH MGC17"
/lab_host="DH10B-R"
/lab_host="DH10B-R"
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Submitted (04-APR-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer
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2283 bp mRNA Homo sapiens, chromosome 20 open reading IMAGE:5104452, mRNA, complete cds. BC027484 BC027484.1 GI:20071610 MGC.
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karyota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; mmalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. (bases 1 to 2283)

NIH-MGC Project URL: http://mgc.nci.nih.gov Contact: MGC help desk Email: cgapbs-r@mail.nih.gov Tissus Procurement: ATCC cDNA Library Preparation: Life Technologies, In cDNA Library Arrayed by: The I.M.A.G.B. Consort DNA Sequencing by: Baylor College of Medicine H Sequencing Center Center code: BCM-HSSC 31 Center Drive, Room 11A03, Bethesda, 3 20892-2590

Web site: http://www.hgsc.bcm.tmc.edu/cdna/ Contact: amg@bcm.tmc.edu Gunaratne, P.H., García, A.M., Lu, X., Huly Yoon, V.S., Kowis, C.R., Lawrence, S., Mart. Hulyk, s Martin, S.W., 1

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    CGTGATCTCAAGCTGTGTCGCTTTGTCTTCGCTGACCGTGAGAGAAGAAGCTGGTGCTG
                                                                                                    GTGCTCTTCCGCCAGATGGCCACCGCCCTGGCGCACTGTCACCAGCACGGTCTGGTCCTG
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Homo sapiens TRB3 protein mRNA,
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Submitted (03-MAR-2003)
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1 (bases 1 to 2488)
Shan, Y. X. and Yu, L.
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Sequence 16 :
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Location/Qualifiers
1. .2116
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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CGTGATCTCAAGCTGTGTCGCTTTGTCTTCGCTGACCGTGAGAGGAAGAAGCTGGTGCTG
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/mol_type="genomic DNA"
/db_xref="taxon:9666"
/note="Incyte ID NO: 1271505CB1"
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                                                                                                        NEDO human cDNA sequencing project supported by Ministry of International Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology; cDNA library construction, 5'- & 3'-end one pass sequencing: Departent of Virology and Human Genome Center, Institute of Medical Science,
                                                                                                                                                                  Submitted (29-AUG-2000) Sumio Sugano, Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure Analysis, Human Genome Center; Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan (B-mail:cdnal@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286, Fax:81-3-5449-5416)
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                                                                                                                                                                                                                                                                                     Kawabata,A., Hikiji,T., Kobatake,N., Inagaki,H., Ikema,Y., Okamoto,S., Okitani,R., Ota,T., Buzuki,Y., Obayashi,M., Nishi,T., Shibahara,T., Tanaka,T., Nakamura,Y., Isogai,T. and Sugano,S. NEDO human cDNA sequencing project
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Homo Bapiens cDNA: FLJ23292 fis,
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                                                                                              University of
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="HRP10334"
/cell_line="HepG2"
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Hafalla,A., Shih,L.L., Tribouley,C.M., Yao,M.G., Burrill,J.D.,
Marcus,G.A., Zingler,K.A., Lu,D.A., Bandman,O., Policky,J.L.,
Griffin,J.A., Thornton,M., Nguyen,D.B. and Walsh,R.T.
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Sequence 21 from Patent
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Direct Submission
Submitted (12-MAR-2001) Division of Genomic Medicine, University Sheffield, Royal Hallamshire Hospital, Floor M, Glossop Road, Sheffield S10-2JF, UK
Sheffield S10-2JF, UK
Location/Qualifiers
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kinase; NIPK.
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Matsuda, K.M., Kojima, S. and Nakayama, T.
Direct Submission
Submitted (09-DEC-1998) Keiko Mayumi Matsuda,
Ltd., Shionogi Institute for Medical Science;
Settsu-shi, Osaka 566-0022, Japan
(8-mail:keiko.matsuda@shionogi.co.jp, Tel:81-6
                                                                                                                                                                                                           Biochem. Biophys. Res. Commun. 258 (2), 260-264 (1999) 99262087
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/codon_start=1
/prodoct="kinase"
/protein_id="BAA77582.1"
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/db_xref="GI:4827159"
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LAPYARLPTHQHVARPTEVLLGSQLLYTFFTKLTGDLHSLVRSRGIPEPEAAALFRQ
MASAVAHCHKSGLILEDLKLRFVPSNCERTKLVLENLEDACVMTGPDDSLMDKHACP
AYUGPELSSRFSYSGRAADVWSLGVALFTMLAGRYPFQDSEPALLFGKIRGTPALP
EGLSASARCLIRCLLRREPSERLVALGILLHPWLREDCSQVSPPRSDRREMDQVVPDG
POLEBAEBEGEVGLYG"
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/note="27 a r
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Pred. No. 4.4e-103;
0; Mismatches 248;
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Best Local Similarity 98.1%;
Matches 622; Conservative
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Novel nucleic acid and amino acid sequences
Patent: WO 0206315-A 57 24-JAN-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Sequence 57 from Patent
AX364906
AX364906.1 GI:18696795
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                                                               CGGGCCTACCGGGCCCTGCACTGCCCTACAGGCACTGAGTATACCTGCAAGGTGTACCCC
                                                                                                                 GCTGTGGCCACTGCCTCCCGTCTTGGGCCCTATGTCCTCCTGGAGCCCCGAGGAGGGCGGG
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                                                                                                   GCTGTGGCCACTGCCTCCCGTCTTGGGCCCCTATGTCCTCCTGGAGCCCGAGGAGGGCGGG
                                                                                                                                                     CCCAGACTGCCCCCCTGTTGCCCCTGAGCCCACCTACTGCTCCAGATCGTGCAACT
                                                                                                                                                                    CCCAGACTGCCCCCTGCCTGTTGCCCCCTGAGCCCAACCTACTGCTCCAGATCGTGCAACT
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  GTCCAGGAAGCCCTGGCCGTGCTGGAGCCCTATGCGCGGCTGCCCCCGCACAAGCATGTG
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                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
352 c 346 g 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
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Pred. No. 1.9e-100;
3; Mismatches 6;
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Novel nucleic acid and amino acid sequences
Patent: WO 0206315-A 72 24-JAN-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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             GTCCAGGAAGCCCTGGCCGTGCTGGAGCCCTACGCGCGGCTGCCCCCCGCACAAGCATGTG
                                                                                              GAGAACCTGGAGGACTCCTGCGTGCTGACTGGGC 634
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GTCCAGGAAGCCCTGGCCGTGCTGGAGCCCTATGCGCGGCTGCCCCCGCACAAGCATGTG
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Location/Qualifiers
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/db_xref="taxon:9606"
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98.1%;
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Patent WO0206315.
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Pred. No. 1.9e-100;
3; Mismatches 6;
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Klausner, R.D., Collins, F.S., Wagner, L., Shaumen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Heich, F.,
Distchenko, L., Marusina, K., Parmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.B., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McBwan, P.J.,
McKerran, K.J., Malek, J.A., Gunaratne, P.H., Richardde, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Pahay, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, B.,
Pahay, J., Helton, E., Ketteman, M., Madan, A., Schwutz, J., Myers, R.M.,
Butfard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.G., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Parasory
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Mus musculus induced in fart
MGC:18731 IMAGE:3980838), cc
BC012955
BC012955.1 GI:15277944
MGC.
Mus musculus (house mouse)
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USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
TWA Commencing by: Baylor College of Medicine Human Genome
                                                                                                                                                                 Strausberg,R.

Direct Submission

Submitsion

Submitted (20-AUG-2001) National Institutes of Health, Mammalian Submitted (20-AUG-2001) National Office, National Cancer Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 1969)
1 (bases 2 colocald R A Grouse, L.H., Derge, J.G.,
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Best Local Sim
Matches 739;
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Clone distribution: MGC clone distribution information can be for through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov geries: IRAK Plate: 23 Row: k Column: 9
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, Similarity but not identity to protein.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged,
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
A.N., Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                CCCAGACTGCCCCCTGCTGTTGCCCCTGAGCCCAACCTACTGCTCCAGATCGTGCAACT
GCCAGCGAGGCCCAGGCGGCTGGCACCTTATGCCCGGCTGCCTACCCACCAGCATGTG
                                          CGGGCCTACCGGGCCCTGCACTGCCCCTACAGGCACTGAGTATACCTGCAAGGTGTACCCC
                                                                                                                                                                                                                                                    GCTGTGGCCACTGCCTCCCGTCTTGGGCCCCTATGTCCTCCTGGAGCCCCGAGGAGGGCCGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /protein_id="AAH12955.1"
/db_xref="G1:15277945"
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EAQAVLAPYARLPTHOHYARPTEVLLGSRFLKYFFTKHVDLERUEDACVMTGSDDSVBAD
GLFROMASAVAHCHHGULLRDLKLRRFVFSBLKYFFALPEGLSAPARCLIRCLLRKEPSB
KHACPAYVGPEILSSRPSYSBPVLLFGKIRRGTFALPEGLSAPARCLIRCLLRKEPSB
KUALGILLHPMLREHGRVSPPQSDRREMDQVVPDGPQLEBABEGEVGLYG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="Mammary tumor. Metallothio model. 10 month old virgin mouse. Taken /clone_libe"NCI_GGAP_Maml" /lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="mRNA"
/strain="FVB/N"
/db xref="taxon:10090"
/clone="MGC:18731 IMAGE:3980838"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="TRB-3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="synonym: TRB-3"
/db_xref="LocuBID:228775"
/db_xref="MGI:1345675"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="Ifld2"
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REPERENCE
AUTHORS
TITLE
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HS1103G7
                               COMMENT
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ORGANISM
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pirect Submission
Submitted (05-PEB-2001) Sanger Centre, Hinxton, Cambridgeshire,
CBIO 15A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
requests: clonerequest@sanger.ac.uk
On Mar 19, 2000 this sequence version replaced gi:5541861.
During sequence assembly data is compared from overlapping clon
                                                                                                                                                                                                                                                                        HS1103G7

HS3170 bp

DNA

linear PRI 08-PBB-2001

Human DNA sequence from clone RP5-1103G7 on chromosome 20p12.2-13.

Contains up to three novel genes, the gene for a novel protein

similar to mouse VMP, the gene for a novel protein kinase domains

containing protein similar to phosphoprotein C8FW and rat NIPK, and

the 60X22 gene for SRY (sex-determining region Y)-box 22. Contains

five CpG islands, ESTs, STSs and GSSs, complete sequence.

AL034548

AL034548

AL034548.25 GI:7263904

HTG; CpG island; NIPK; protein kinase; SOX22; SRY; VMP.
                                                                                                                                                              Eukaryota, Metazoa, Chordata, Mammalia, Eutheria, Primates, (bases 1 to 153170)
                                                                                                                                             Blakey,S.
                                                                                                                                                                                                                                    Homo sapiens
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RP5-1103G7 is from the library RPCI-5 constructed by the Spiter de Jong. For further details see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that traition annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences only a small overlap as described above.
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Em:, EMBL; Sw:, SWISSROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      http://www.chori.org/bacpac/home.htm
                                                                                                                                                                             2938. .3062
/note="L1M4 repeat: matches 3120. .3249 of consensus"
3136. .3430
/note="AluSg repeat: matches 1 ~~~
3482. .3777
                         4310. 4608
/note="LIMD2 repeat: matches 5861. .6167 of consensus"
4609. .5026
                                                                                                                                                                                                                                                                                          complement (join(2194. .2243,126792. .126871))
/note="match: GSS: Em:AQ377604"
2699. .2917
/note="LIM4 repeat: matches 2875. .3081 of co
2938. .3062
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="LIMA9 repeat: matches 5519. 902. .1109
                                                                                                                                                                                                                                                                                                                                                                                                                                                              2154. .2193
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1734. .1888
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                                                                                                                                                                                                                                                                                                                                                                                                                             /note="20 copies 2 mer as 85% conserved"
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/db_xref="taxon:9606"
/chromosome="20"
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mol_type="genomic DNA"
repeat:
matches 1. .424 of consensus"
                                                                                                                                                            matches 1.
                                                                                                       matches 1. .312 of consensus"
                                                                                                                                                            .296 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .547 of consensus"
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                                                                                                                                                                                                                                                                     /note="LIMA5 repeat: matches 5947. .6300 of 10488. .10529
/note="21 copies 2 mer at 88% conserved" 10532. .10653
/note="LIMC4 repeat: matches 7673. .7800 of 10687. .10752
/note="33 copies 2 mer at 68% conserved" 11681. .11742
/note="31 copies 2 mer ta 71% conserved" 13519. .13972
                                                                                               /note="LTR16B repeat: matches 110...462 of consensus"
15554...15872
/note="LTR17 repeat: matches 5615...5910 of consensus"
15873...16174
/note="Alusp repeat: matches 16...313 of consensus"
16175...16382
/note="LINKI repeat: matches 5400...5615 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                      9653. 9750
/note="LIMA5 repeat: matches 5856. .5947 of consensus"
9751. .10047
/note="AluSx repeat: matches 1. .298 of consensus"
10048. .10369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9226. .9311
/note="L1MB4 repeat: matches 5775. .5862 of consens
9312. .9651
/note="MER1B repeat: matches 1. .337 of consensus"
                  /note="Aluy repeat: matches 1. .302 of consensus"
16895. .17021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8943. .9113
/note="MER4D repeat: matches 194. .362 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8349. .8643 repeat: matches 362. .689 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8019. .8317
/note="match: GSS: Em:AQ746749"
8019. .8151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="30 copies 2 mer ca 88% conserved"
6710. .6824
/note="MERSO repeat: matches 10. .134 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="LIMD2 repeat: matches 5684. .5861 of consensus" 5201. .5501 /note="RIMD2 repeat: matches 1. .307 of consensus" 5502. .5727 /note="LIMD2 repeat: matches 5451. .5684 of consensus"
                                                                                                                                                                                                                           13519. .13972
/note="match: GSS: Em:AQ224309"
14208. .14554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8644. .8942
/notes"AluY repeat: matches 1. .299 of consensus"
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                                                                   note="LIMB repeat:
'note="L1MA10 repeat: matches 6196. .6318 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        )113. .9201
/note="MLT2FA repeat: matches 377. .450 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note⇒"MBR4B repeat: matches 416. .574 of consensus"
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/note="match: GSS: Em:AQ123077"
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/note="match: GSS: Em:AQ180303"
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note="LIMA4A repeat: matches 5619.
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AGGGAAGAGGGAGACAGAGAAGTGGTTCTGTATGGC 151365
                              AGGGAAGAGAGAGAGAGAGTGGTTCTGTATGGC 1074
                                                                           CGATCCCATCTCTGGGAGGCTGCCCAGGTGGTCCCTGATGGACTGGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="MLTIE repeat: matches 256. .421 of consensus" 20895. .21012 / 20895. .21012 / 20895. .21018 of consensus / 20896. .-1108 of consensus / 20896. .21168
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17897. .18157
1700ce="LIM1 repeat: matches -1389. .-790 of consensus"
18158. .18195
/note="19 copies 2 mer tg 97% conserved"
18197. .18230
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Pred. No. 5.5e-82;
0; Mismatches 15; Indels 0;
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Search completed: January 16, 2004, 14:49:08 Job time: 4032.84 Becs

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Match Length DB
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10840.821 Million cell updates/sec
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	COMMENT	TITLE	AUTHORS	REFERENCE			ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION		DEFINITION	LOCUS	RESULT 1 AL578892/c
Contact: Genoscope Genoscope - Centre National de Sequencage Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - France Bmail: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 10000.f For more information about this cluster, see http://www.genoscope.cns.fr/ cgi-bin/cluster.cgi?seq=CSODK005AB03NPl&cluster=10000.f. Contact : Feng Liang Email: fliang@lifetech.com URL:	Unpublished On Feb 16, 2001 this sequence version replaced gi:12943405.	Full-length cDNA libraries and normalization	Li, W.B., Gruber, C., Jessee, J. and Polayes, D.	1 (bases 1 to 1201)	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,	Homo sapiens	Homo sapiens (human)	BST.	AL578892.2 GI:31317080	AL578892	cDNA clone CS0DK005YC05 3-PRIME, mRNA sequence.	AL578892 Homo gapiens HELA CELLS COT 25-NORMALIZED Homo gapiens	AL578892 1201 bp mRNA linear BST 01-JUN-2003	

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                                                                 TGGGAACTGTGTTCCCAGCATCTCTGTCCTCTTGATTAAGAGATTCTCCTTCCAGGCCTA 170:
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ilarity 96.1%;
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/note="let strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
a 298 c 288 g 246 t 84 others
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/mol type="mRNA"
/db_xref="texon:9606"
/clone="CSODK005YC05"
/cell type="HELA CELLS COT 25-NORMALIZED"
/cell line="HELA"
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24; Mismatches 13;
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Genoscope Centre National de Sequencage
BP 191 91006 KYRY cedex - France
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 10000.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DB003CH10NP1&cluster=10000.f. Contact
Feng Liang Email: fliang@lifetech.com URL:
http://filllength.invitrogen.com/ InVitroGen Corporation 1600
Faraddy Avenue Genoscope sequence ID: CS0DB003CH10NP1.
Location/Qualifiers
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Mammalia; Butheria;
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CDNA Clone CSODB003YP19 3-PRIME, mRNA sequence.
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GGGAGACAGAGAGAGTGGTTCTGTATGGCTAGGACCACCCTACTACACGCCTCAGCTGCCAA 1154
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/clone_lib="Homo sapiens NEUROBLASTOMA COT 10-NORMALIZED"
/note="Tist strand cDNA was primer that sold cDNA was primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and BcoR V sites of the PCMVSPORT 6 vector. Library was normalized."
a 248 c 243 g 210 t 17 others
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Primates;
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Pred. No. 1.7e-73;
9; Mismatches 19
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Bukaryota, Metazoa, Chordata, Craniata, Vert Mammalia, Butheria, Primates, Catarrhini, Ho 1 (bass 1 to 1075)
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Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 10000.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSOAL002CE04NP1&cluster=10000.f. Contact
Peng Liang Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Paraday Avenue Genoscope sequence ID: CSOAL002CE04NP1.
Location/Qualifiers
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Genoscope - Centre National de Sequencage
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                                                  CCATAGGTCACTGTCTACACTGGGTACACTTTGTACCAGTGTCGGCCTCCACTGATGCTG
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/cell_line="RAMOS CELL LINE"
/clone_lib="Homo sapiens B CELLS (RAMOS CELL LINE) COT
25-NORMALIZED"
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/mol_type="mRNA"
/db_xref="taxon:9606"
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10; Mismatches 30
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Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 10000.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi.bin/cluster.gi?req=cgoDC013DE04NP1&cluster=10000.f. Contact
Feng Liang Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CSODC013DE04NP1.
Location/Qualifiers
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1 (bases 1 to 1051)

Li.W.B., Gruber,C., Jessee,J. and Polayes,D.
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                                           /organism="Homo sapiens"
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/db_xref="texxon:9606"
/clone="CSODCO13YJO8"
/clone="CSODCO13YJO8"
/clone="Ibs"-Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED"
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                 BAAAATSCCVGGTCNATAGTNTAGGTATT-GATRCGAGGAGWAKRKAKR
                                                                          GTCTGTCCTGTGGCCACCTGGAAAGTCCCAGGTGGGACTCTTCTGGGGACACCTTGGGGTC 1909
                                                                                                                    GCCTBTCAACCATGGGGCTTCTGACCTGAGCACCAAGGTTGAGGGACAGGATTAGGCAGG
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BX325344 Homo sapiens B CELLS (RAMOS CE

RNA linear CBLL LINB) COT

EST 02-MAY-2003 25-NORMALIZED

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            AGATGACAAACTGGCATCCTTGAGCTGACAACACTTTTCCATGACCATAGGTCACTGTCT 1449
                                                              CCTGTTCTCGGTGCTGGGAGTACAGCAGTGAGCAAAGGAGACAATATTCCCTGCTCACAG 1385
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llarity 96.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/mol type="mRNA"
/mol type="mRNA"
/db xref="taxon:9606"
/clone="CSODL004YF04"
/cell type="B CELLS (RAMOS CELL LINE) COT 25-NORWALIZED"
/cell line="RAWOS CELL LINE"
                                                                                                                                                                                                                                                                                                                          ; Score 892; DB 13;
; Pred. No. 1.4e-72;
22; Mismatches 10;
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                                                                                                                                                                             Contact: Robert Strausberg, Ph.D. Bmail: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
                                                                                                                                                                                                                           1 (bases 1 to 975)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
                                                                                                                                                                                                                                                                                                                         mRNA sequence. BG575275
BG575275
BG575275.1 GI:13582928
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                                                                     quality sequence stop: 891.
Location/Qualifiers
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Primates;
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CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLN DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov plate: LLAN10575 row: a column: 08 High quality sequence stop: 891.
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/organiam="Homo sapiens"
/mol_type="mRNA"
/db xrefs"ttaxon:9606"
/dlone="IMAGB:4706575"
/tlssue_type="mammary adenocarcinoma, cell line"
/lab host="DH108 (phage-resistant)"
/clone_lib="NHH_MGC_87"
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  TCCCCTGCAACTCAGGACCCAAGCCCAGCTCACTCTGGGAACTGTGTTCCCAGCATCT 1666
                       GGTATCCTGTACCTTTTCAAGATAAGGGGAGGAATCCCTGGGGCAAAGGCTTCCAGGCTC
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Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 10000.f.
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSODCO13CE11NP1&cluster=10000.f. Conta-
feng Liang Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com/Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID: CSODCO13CE11NP1.
Location/Qualifiers
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AL562576 GI:31286588
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1 (Dases 1 to 1001)

Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
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BP 191 91006 EVRY cedex - France
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Mammalia; Butheria;
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ACACATCTGCTTTGTTCCACACA-CATGCAGTTCCTGCTTGGGTGCTTATCAGGTGCCAA
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/clone_Tib="Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED"
/note="Tist strand cDNA was primed with a NotI-oligo(dT)
primer Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and BcoR v
sites of the pCMYSPORT 6 vector. Library was normalized."
a 250 c 257 g 224 t 40 others
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/mol_type="mRNA"
/db_xref="taxon:9606"
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tive 33; Mismatches
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5', mRNA Bequence.
BQ216198
BQ216198.1 GI:20397598
EST.
  Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP/Gazdar

cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
                                                                                                                                    Bukaryota; Metazoa; Chordata; Craniata; \Mammalia; Butheria; Primates; Catarrhini; 1 (bases 1 to 873)
NIH-MGC http://mgc.nci.nih.gov/.
Mational Institutes of Health, Mammalian
                                                                                                                           Unpublished
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/tissue_type="large_cell carcinoma"
/lab_host="DH108 (phage-resistant)"
/clone_lib="WIH_MGC_68"
/note="Organ: lung; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT.
Average_insert_size_1.8 kb. Library_constructed_by_Life_Technologies."
a 305 c 264 g 160 t
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/mol_type="mRNA"
/db_xref="taxon:9606"
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Pred. No. 1.1e-68;
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1 (bases 1 to 881)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.B. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2599 row: p column: 17
High quality sequence stop: 689.
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AGENCOURT_8821009 NIH_MGC_18 Homo
5', mENA sequence.
B0941789
B0941789.1 GI:22357267
EST.
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Tissue Procurement: DCTD/DTP/Gazdar
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Robert Strausberg, Ph.D.
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                        GAACCTGGAGGACTCCTGCGTGCTGACTGGGCCAGATGATTCCCTGTGGGACAAGCACGC
                                         GAACCTGGAGGACTCCTGCGTGCTGACTGGGCCAGATGATTCCCCTGTGGGACAAGCACGC
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/tissue_type="large cell rearsistant)"
/clone_lib="NIH MGC_18"
/clone_lib="NIT Constructed by Ling Hong in the into EcoRI/KhoI sites using the following 5' adaptor:
GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superseript II RT (Life Technologies). Note: this is a NIH_MGC Library."
61 a 275 c 262 g 181 t 2 others
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Email: segref@genoscope.cns.fr, Web: www.genoscope.cns.fr Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 10000.f more information about this cluster, see http://www.genoscope.cns.fr/
                                                                                     Mammalia; Butheria; Primates; Catarrhini; Ho; 1 (bases 1 to 945)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization unpublished
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 9106 EVRY cedex - France
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BX325345 Homo sapiens B
Homo sapiens cDNA clone
BX325345
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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                CGTGCTGACTGGGCCAGATGATTCCCTGTGGGACAAGCACGCGTGCCCAGCCTACGTGGG
                                                                                                                 CACCGCCCTGGCGCACTGTCACCAGCACGGTCTGGTCCTGCGTGATCTCAAGCTGTGTCG
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/Cell_type="B CELLS (RAMOS CELL LINE) COT 25-NORWALIZED"
/Cell_line="RAMOS CELL LINE"
/Clone_lib="Homo sapiens B CELLS (RAMOS CELL LINE) COT 25-NORWALIZED"
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al Similarity 89.5%;
949; Conservative 21
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Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 10000.f
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSOAHOOICAO6NP1&cluster=10000.f. Conta
Peng Liang Email: fliang@lifeteh.com URL:
http://fullength.invitrogen.com/. InVitroGen Corporation 1600
Paraday Avenue Genoscope sequence ID: CSOAHOOICAO6NP1.
Location/Qualifiers
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1 (bases 1 to 1201)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Pull-length cDNA libraries and normalization
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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                 GCGYTTYTGTTRSTKCTCCTCGTCGGAGCAGCTGACGCTAACACAACAGCATCTTCTGS
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GCCCAGAKGTCCCTGWTTTAYT-GGGCTGGACGAAGCCAGGGAAGAGAGGGAAGACAGAG
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                                                                                                                                                                                                                                                                                                         /organisma"Homo sapiens"
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/db_xref="taxon:9606"
/clone="CSODH001YB11"
/tissue_type="T CELLS (JURKAT CELL LINE)"
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/clone_lib="Homo sapiens T CELLS (JURKAT CELL LINE)"
/clone_lib="Homo sapiens T CELLS (JURKAT CELL LINE)"
/clone_lib="Homo sapiens T cells strand cDNA was primed
/note="Vector: pCMVSPORT 6; lst strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned int
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."
52 others
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11; Mismatches 81;
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Bmail: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr

Invitrary was constructed by Life Technologies, a division of

Invitrogen. This sequence belongs to sequence cluster 10000.

more information about this cluster, see

http://www.genoscope.cns.fr/

cgi-bin/cluster.cgi/seq=CSIDH001ZB03NP1&cluster=10000.f. Con

Peng Liang Email: fliang@lifetech.com URL:

http://fulllength.invitrogen.com/ InvitroGen Corporation 160

Paraday Avenue Genoscope sequence ID: CSIDH001ZB03NP1.

Location/Qualifiers
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Contact: Genoscope
Genoscope - Centre National de Sequencage
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1 (bases 1 to 1201)
Li,W.B., Gruber.C., Jessee,J. and Polayes,D.
Pull-length cDNA libraries and normalization
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                GGAGACAATATTCCCTGCTCACAGAGATGACAAACTGGCATCC-TTGAGCTGACAACAC-
                                                                                                                                                                                  GACCACCCTACTACACGCTCAGCTGCCAACAGTGGGATTGAGTTTGGGGGGTAGCTCCAAGC
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                                                            TTGGGTGCTTWTCAGGTGCCAAGCCCTGTTCTCGGTGCTGGGAGCACAGCAGTGAGCAAA
                                                                            TTGGGTGCTTATCAGGTGCCAAGCCCTGTTCTCGGTGCTGGGAGTACAGCAGTGAGCAAA
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODH001YB11"
/tissue_type="T CELLS (JURKAT CELL LINE)"
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/clone_lib="Homo sapiens T CELLS (JURKAT CELL LINE)"
/clone_lib="Homo sapiens T CELLS (JURKAT CELL LINE)"
/clone_lib="Homo sapiens T CELLS (JURKAT CELL LINE)"
/clone_rector: pCMVSPORT 6; 1st strand cDNA was primed
/note="Vector: pCMVSPORT 6 vector.
/clone_library was not normalized."

53 a 292 c 303 g 245 t 98 others
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                                                                                                      found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLCM1676 row: i column: 13
                                                                                                                                                                                     Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health,
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602705453F1 NIH_MGC_43 Homo sapiens
                                                                                                                                                                                                             Contact: Robert Strausberg,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                     cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can
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Location/Qualifiers
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/note="Organ: eye; Vector: pOTB7; Site_1: xhoI; Site_2: /note="Corgan: eye; Vector: pOTB7; Site_1: xhoI; Site_2: /note="Corgan: eye; Vector: pormaing. Directionally cloned into EccRI/KhoI sites using the following 5; cloned into EccRI/KhoI sites using the following 5; adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH MGC Library. | "
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GCCACTACCCCTTCCAGGACTCGGAGCCTGTCCTGCTCTTCGGCAAGATCCGCCGCGGGG ACTCGGGCAAGGCAGCCGATGTCTGGAGCCTGGGCGTGGCGCTCTTCACCATGCTGGCCG GGGACAAGCACGCGTGCCCAGCCTACGTGGGACCTGAGATACTCAGCTCACGGGCCTCAT GGGACAAGCACGCGTGCCCAGCCTACGTGGGACCTGAGATACTCAGCTCACGGGCCTCAT AGCTGGTGCTGGAGAACCTGGAGGACTCCTGCGTGCTGACTGGGCCAGATGATTCCCTGT AGCTGGTGCTGGAGAACCTGGAGGACTCCTGCGTGCTGACTGGGCCAGATGATTCCCTGT GTCTGGTCCTGCGTGATCTCAAGCTGTGTCGCTTTGTCTTCGCTGACCGTGAGAGGAAGA TCACTCGGACCCATGGGGACATGCACAGCCTGGTGCGAAGCCGCCACCGTATCCCTGAGC ACAAGCATGTGGCTCGGCCCACTGAGGTCCTGGCTGCTACCCCAGCTCCTACGCCTTTT AGGTGTACCCCGTCCAGGAAGCCCTGGCCGTGCTGGAGCCCTACGCGCGGGTGCCCCCGC ATCGTGCAACTGCCTGTGGCCACTGCCTCCCGTCTTGGGCCCCTATGTCCCTCCTGGAGCCCG GGCGCGGCCAGATGCGAGCCACCCCTCTGGCTGCTCCTGCGGGTTCCCTGTCCAGGAAGA ACTCGGGCAAGGCAGCCGATGTCTGGAGCCTGGGCGTGGCGCTCTTCACCATGCTGGCCG GTCTGGTCCTGCGTGATCTCAAGCTGTGTCGCTTTGTCTTCGCTGACCGTGAGAGGAAGA CTGAGGCTGCCGTGCTCTTCCGCCAGATGGCCACCGCCCTGGCGCACTGTCACCAGCACG CTGAGGCTGCCGTGCTCTTCCGCCAGATGGCCACCGCCCTGGCGCACTGTCACCAGCACG TCACTCGGACCCATGGGGACATGCACAGCCTGGTGCGAAGCCGCCACCGTATCCCTGAGC ACAAGCATGTGGCTCGGCCCACTGAGGTCCTGGCTGGTACCCAGCTCCTCTACGCCTTTT AGGTGTACCCCGTCCAGGAAGCCCTGGCCGTGCTGGAGCCCTACGCGCGGCTGCCCCCGC AGGAGGGCGGGCCTACCGGGCCCTGCACTGCCCTACAGGCACTGAGTATACCTGCA AGGAGGGCGGGCCGTACCGGGCCCTGCACTGAGTATACCTGCA ATCGTGCAACTGCTGTGGCCACTGCCTCCCGTCTTGGGCCCTATGTCCTCCTGGAGCCCG GTGGGCCCAGCCCAGACTGCCCCCCCTGCCTGTTGCCCCTGAGCCCACCTACTGCTCCAG GTGGGCCCAGCCCAGACTGCCCCCCCTGCCTGTTGCCCCTGAGCCCACCTACTGCTCCAG AGCGGTTGGAGTTGGATGACAACTTAGATACCGAGCGTCCCGTCCAGAAACGAGCTCGAA AGCGGTTGGAGTTGGATGACAACTTAGATACCGAGCGTCCCGTCCAGAAACGAGCTCGAA GACGGGGGGAGATGCGAGCCACCCCTCTGGCTGCTCCTGCGGGGTTCCCTGTCCAGGAAGA Conservative 39.8%; <u>.</u>. Score 818.6; DB 1 Pred. No. 6.6e-66; 0; Mismatches 14 DB 10; 14; Length 863; 1, Gaps 850 877 637 517 191 131 157 791 817 731 671 697 611 577 457 311 337 251 217 71 757 551 431 371 397 277 97 491

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cgi-bin/cluster-gj?seq=CSGDX05AB03QP1&cluster=10000.f. Conti-
cgi-bin/cluster.cgi?seq=CSGDX05AB03QP1&cluster=10000.f. Conti-
Peng Liang Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com/ Invitroden Corporation 1600
Paraday Avenue Genoscope sequence ID: CSODK005AB03QP1.
Location/Qualifiers
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BP 191 91006 EVRY cedex - France
Bmail: seqref@genoscope.cns.fr; Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 10000.f
more information about this cluster, see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished
On Peb 15, 2001 this sequence version replaced
Contact: Genoscope
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Li.W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished
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Mammalia; Butheria; Primates; Catarrhini; Hominidae;
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                                                             Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 10000.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSDDC007CC03QP1&cluster=10000.f. Contact
Feng Liang Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CSODG007CC03QP1.
Location/Qualifiers
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Pull-length cDNA libraries and normalization Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               948 bp mRNA line SX443303 Homo sapiens B CELLS (RAMOS CELL LINE) Clone CSODG007YF05 5-PRIME, mRNA sequence.
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Genoscope - Centre National de Sequencage
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/tiesue_type="B_CELLS (RAMOS_CELL_LINE)"
/cell_line="RAMOS_CELL_LINE"
/cell=line="RAMOS_CELL_LINE"
/clone_lib="Homo sapiens_B_CELLS (RAMOS_CELL_LINE)"
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Library was not normalized."
52 a 326 c 296 g 169 t 5 others
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Copyright (c) 1993 - 2004 Compugen Ltd.
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                                 22-MAR-2001.
                                                                                  misc_feature
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Best Local Similarity
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09-JUL-2000; 2000US-05598042.
19-JUL-2000; 2000US-0620312.
03-AUG-2000; 2000US-0653450.
14-SEP-2000; 2000US-0653191.
19-CCT-2000; 2000US-0693036.
29-NOV-2000; 2000US-0727344.
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  WPI; 2001-442253/47
P-PSDB; AAM40694.
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The invention relates to human nucleic acids (AAI57798-AAI61369) and CC the encoded polypeptides (AAM38642-AAM4221)) with nootropic, immunosuppressant and cytostatic activity. The polynuclectides are useful CC in gene therapy. A composition containing a polypeptide or polynuclectide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and CC localised neuropathies and central nervous system diseases, such as CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the CC utilisation of the activities such as: Immune system diseases, haemostatic activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic CC and thrombolytic activity, cancer diagnosis and therapy, drug screening, CC assays for receptor activity, arthritis and inflammation, leukaemias and CC utilisation of the sequence data for this patent did not form part of the printed cyc specification.
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Sequence 2059 BP; 400 ₽ 645 C; 583 G; 431 T; 0 other;

Similarity

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14-SEP-2000;
19-OCT-2000;
29-NOV-2000;
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(HYSE-)
HYSEQ INC.
                          7 2000US-0488725.

7 2000US-0552317.

9 2000US-0598042.

1 2000US-0620312.

1 2000US-0653450.

1 2000US-0653151.

2 2000US-0693036.

2 2000US-0727344.
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Novel nucleic Ş, Ţ 2001-442253/47 DB; AAM38908. central nervous Wang 2 Zhou , so Asundi V, Wehrman T, Goodrich F polypeptides, useful system injuries -Chen R, Ma Y,
, Xu C, Xue AJ,
R, Drmanac RT; æ Qian 1 Ren F, Zhang disorders ٦ Wang

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Claim 1, SBQ ID NO 267; 10078pp; English.

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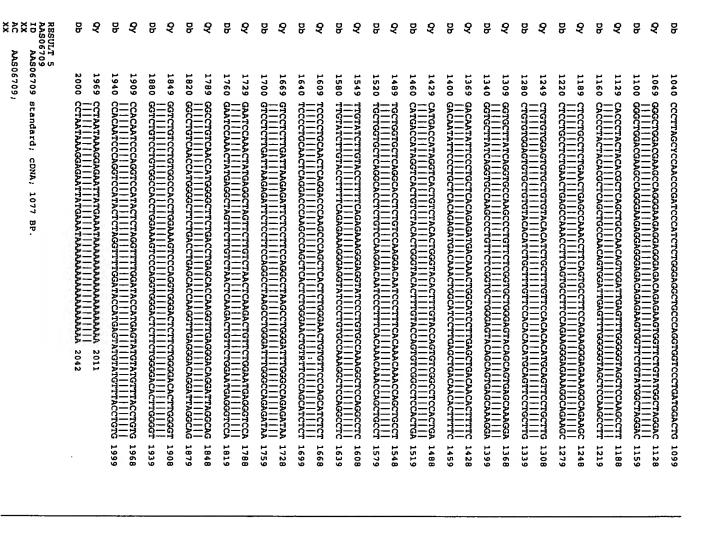
The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polypnucleotides are useful in gene therapy. A composition containing a polypeptide or polypnucleotide of the invention may be used to treat diseases of the peripheral nervous

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871 TGBAGCCTGGGCGTGGCCCTTCACCATGCTGGCCGGCCACTACCCCTTCCAGGACTCG 930		811 TACGTGGGACCTGAGATACTCAGCTCACGGGCCTCATACTCGGGCAAGGCCGATGTC 870	<u> АССТОСОВАССТВАСАТАСТСАССТСАССОССТСАТАСТСОССЕДА ОССТОВЕНИЕ</u>	751 GACTCCTGCGTGCTGACTGGGCCAGATGATTCCCTGTGGGACAAGCACGCGTGCCCAGCC 720	91 CTGTGTCGCTTTGTCTTCGCTGACACGTGAGAAGAAGCTGGTGCTGGAGAAACCTGGAG 75	01 CTGTGTCGCTTTGTCTTCGCTGACCGTGAGAGGAAGAAGCT;XGCTGGAGAACCTXGAG 6	631 CAGATGGCCACCGCCCTGGCGCACTGTCACCAGCACGGTCTGGTCCTGCGTGATCTCAAG 690	1 CACAGCCTGGTGCGAAGCCGCCACCGTATCCCTGAGCCTGAGGCTGCCGTGCTCTTCCGC 63	81 CACAGCCTGGTGCGAAGCCGCCACCGTATCCCCTGAGCCTGAGGCTGCGCGTGCTCTTCCGC 54	11 GAGGTCCTGGCTGGTACCCAGCTCCTCTACGCCTTTTCACTCGGACCCATGGGGACATG 57	21 GAGGTCCTGGCTGGTACCCAGCTCCTCTACGCCTTTTTCACTCGGACCCATGGGAACATG	361 CTGGCCGTGCTGGAGGCCCTACGCGCGCGCCGCACAAGCATGTGGCTCGGCCCACT 420	유=	CCCTGCACTGCCCTACAGGCACTGAGTATACCTGCAAGGTGTACCCCGT	31 GCCTCCCGTCTTGGGCCCTATGTCCTCCTGGAGCCCGAGGAGGGCGGGC	41 GCTTCCCTTTTCCCCTTTTTTCTCCTTCTTCTTCTTCTTC	181 CCCTGCCTGTTGCCCCTGAGCCCACCTACTGCTCCAGATCGTGCAACTGCTGTGGCCACT 240	CGAGCGTCCCGTCCAGAAACGAGCTCGAAGTGGGCCCCAGCCCAGACTC	121 TTAGATACCGAGCGTCCCGTCCAGAAACCGAGCTCGAAGTGGGCCCCAGCCCAGACTGCCC 180		61 CCTCTGGCTGCTGCGGGTTCCCTGTCCAGGAAGAGGGGTTGGAGTTGGATGACAAC 120	1 GCTCTGAGCCCCGGGGGCCCCAGGCCCACGCGGAACGACGGGGCGAGATGCGAGCCACC 60	Duery Match 97.0%; Score 1997.2; DB 22; Length 2092; Best Local Similarity 99.9%; Pred. No. 0; Matches 1999; Conservative 0; Mismatches 3; Indels 0; Gaps 0;	Sequence 2092 BP; 405 A; 658 C; 593 G; 436 T; 0 other;	Note: The sequence data for this patent did not form part of the printed specification.	reening nias an	nosta	system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic	

europathy and	१	841 GAGCCTGTCCTGCTCTTCGGCAAGATCCGCCGCGGGGCCTACGCCTTGCCTGCAGGCCTC 900
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                                                                                                                                                                                                                                                                                                                                                                       Claim
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Plowman GD,
Flanagan P,
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                                                                                                                                                                      WPI; 2001-343950/36.
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Nucleic acids encoding human kinase polypeptides, useful for preventing diagnosing and/or treating e.g. cancer, immune, cardiovascular and neuronal-associated diseases, and microbial infections -

Example 1; Figure 1; 433pp; English.

CC AASO6701-AASO6757 encode for novel human protein kinases #1-57. The CC novel protein kinases have been identified as members of the tyrosine CC or serine/threonine kinase (PTK and STK) families. The polynucleotides CC encoding protein kinases and the polypeptides may be used in the CC prevention, diagnosis and treatment of diseases associated with CC inappropriate kinase expression. For example, they may be used to treat CC cancers (especially cancers of haematopoietic origin), cardiovascular CC disease (e.g. atherosclerosis), metabolic disorders (e.g. diabetes), CC immune related diseases (e.g. rheumatoid arthritis), neurological CC disorders (e.g. schizophrenia), neurodegenerative disorders (e.g. Gratkinson's disease), inflammatory disorders (e.g. asthma), infectious CC disease (e.g. HIV) and reproductive disorders (e.g. asthma), infectious CC disease (e.g. HIV) and reproductive disorders (e.g. asthma), infectious CC used for gene therapy and as DNA probes in diagnostic assays. CC used for gene therapy and as DNA probes in dispositic assays. CC of antibodies against the protein kinases and in assays to identify condulators of protein kinase expression and activity.

Sequence 1077 BP; 174 A; 373 C; 325 G; 205 T; 0 other;

ঠ ঠ 문 밁 밁 र् 밁 ঠ Query Match Best Local Similarity Matches 1075; Conserv 229 121 169 181 109 13 49 -CCCAGACTGCCCCCCTGCCTGTTGCCCCCTGAGCCCCACCTACTGCTCCAGATCGTGCAACT GCTGTGGCCACTGCCTCCCGTCTTGGGCCCTATGTCCTCCTGGAGCCCCGAGGAGGGCCGG CCCAGACTGCCCCCCTGCCTGTTGCCCCTGAGCCCCACCTACTGCTCCAGATCGTGCAACT TTGGATGACAACTTAGATACCGAGCGTCCCGTCCAGAAACGAGCTCGAAGTGGGCCCCAG TTGGATGACAACTTAGATACCGAGCGTCCCGTCCAGAAACGAGCTCGAAGTGGGCCCCAG ATGCGAGCCACCCCTCTGGCTGCTCCTGCGGGTTCCCTGTCCAGGAAGAAGCGGTTGGAG ATGCGAGCCACCCCTCTGGCTGCTCCTGCGGGTTCCCTGTCCAGGAAGAAGCGGTTGGAG Conservative 52.2**%**; ; Score 1073.8; pred. No. 6e-1: 0; Mismatches DB 22; <u>ب</u> Indels Length 1077; . Gape 288 240 120 60 180 228 168

AAS06709, AAS06709

standard;

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           Human; tribbles; htrb-1; stress kinase inhibitor protein; SKIP-1; AP-1; antifrheumatic; antiarthritic; antidiabetic; antipsoriatic; osteopathic; opthalamological; cardiant; cytostatic; haemostatic; immunosuppressive; antiinflammatory; estrogen receptor; fibroblast growth factor; FGF; tumour necrosis factor; TNP; gene; htrb-3; ds.
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                                                                                  tribbles homologue-3 (htrb-3)
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                                                                                                                                                                                                              The invention provides an isolated human tribbles homologue-1 (htrb-1, CC also known as stress kinase inhibitor protein (SKIP-1)) polypeptide. The CC htrb polypeptide is useful for inhibiting an AP-1 mediated inflammatory (Signal in a cell. The polypeptide employed in the method is preferably (CC htrb-1, htrb-1 N htrb-1 C, htrb-1 N C, htrb-3 N trb-3). Ntrb-3 C, or CC htrb-3 N C. It is also useful for providing htrb agonist activity for CC activating an ERK-mediated signal e.g. AP-1-mediated gene activation (CG signal, an estrogen receptor-mediated gene activation signal, an CC fibroblast growth factor (FGP) induced signal, or a PMA induced signal, an CC fibroblast growth factor (FGP) induced signal, or a PMA induced signal, or a fibroblast growth factor (FGP) induced signal, or a pmd induced signal, or a fibroblast growth factor (FGP) induced signal, or a pmd induced factor (TNF) (CC induced inflammatory signal, or an interleukin induced inflammatory signal, or an interleukin induced inflammatory compounds e.g. for treating and/or preventing diseases caused by abnormal htrb activity, such as rheumatoid arthritis, diseases caused by abnormal htrb activity, such as rheumatoid arthritis, diseases caused CC psoriasis, osteoporosis, diabetic retinopathy, myocardial infarction CC and cancers. The htrb therapeutics are useful for antagonizing CC interleukin-1 dependent disorders of human placenta, intraventricular hemorrhage, neonatal white matter damage and subsequent cerebral palsy, a nording reaching reaching disorders. The present sequence represents
                                                                                                                                       Query Match
Best Local Sim:
Matches 1073;
                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel isolated human tribbles homologue-1 polypeptide for inhibiting AP-1-mediated inflammatory signal in a cell, and activating ERK-mediated signal e.g. AP-1-mediated gene activation signal in a ce
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TTGGATGACAACTTAGATACCGAGCGTCCCGTCCAGAAACGAGCTCGAAGTGGGCCCCCAG
                   TTGGATGACAACTTAGATACCGAGCGTCCCGTCCAGAAACGAGCTCGAAGTGGGCCCCAG
                                                                   ATGCGAGCCACCCCTCTGGCTGCTCCTGCGGGTTCCCTGTCCAGGAAGAAGCGGTTGGAG
                                                                                            ATGCGAGCCACCCCTCTGGCTGCTCCTGCGGGTTCCCTGTCCCAGGAAGAAGCGGTTTGGAG
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ilarity 99.1%;
Conservative
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                                                                                                                                                                                                                                               the htrb-3 polypeptide.
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/product= "htrb-3"
/note= "tribbles p
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                                                                                                                                       Score 1054.6;
Pred. No. 1.5e
0; Mismatches
                                                                                                                                                                                                            327 G;
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        of a protein kinase.
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04-AUG-1998;
11-SEP-1998;
                                                                                                                                                                                                                   Kinase activity; molecular weight marker; isoelectric focusing marker; peptide fragmentation control; cellular signal transduction; ss.
                                                                                                                                                      03-AUG-1999;
                                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                          WO200008180-A2
                                                                                                                                        98US-0095270.
98US-0099972.
                                                                                                                                                      99WO-US17630
                                                                                                                                                                                           Location/Qualifiers
2..1081
                                                                                                                                                                                   "partial sequence"
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New human kinase polypeptides and polynucleotides used as molecular weight markers and as controls for peptide fragmentation

WPI; 2000-195584/17. P-PSDB; AAY69157.

Virca

9

Bird

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Anderson

7

Marken

(IMMV) IMMUNEX CORP

Claim ۲, Page 7; 60pp; English

The present sequence encodes a partial polypeptide which has kinase activity. The kinase polynucleotides can be used to express the polypeptides, and as probes to identify nucleic acids encoding proteins having kinase activity. The kinase polypeptides and controls for peptides fragmented polypeptides are used as molecular weight and isoelectric focusing markers, and as controls for peptide fragmentation. They also have a number of therapeutic uses as kinases play a central role in cellular signal transduction. The polypeptides could also be used to identify binding partner proteins. The polypeptides can also be used as a reagent to identify any proteins that the polypeptide regulates, and proteins with which it might interact. The polypeptides may also be used for preparation of antibodies. The antibodies can be used in assays to detect the presence of the protein, and to purify the protein by immunosffinity chromatography.

Sequence 1085 BP; 164 A; 389 C; 338 G; 194 T; 0 other;

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Query Match
Best Local Similarity
Matches 1005; Conserv
  320
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              CCCTGCCTGTTGCCCCTGAGCCCACCTACTGCTCCAGATCGTGCAACTGCTGTGGCCACT
                                                                   CCCTGCCTGTTGCCCCTGAGCCCACCTACTGCTCCAGATCGTGCAACTGCTGTGGCCACT
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Conservative
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Pred. No. 1.1e-168;
0; Mismatches 1;
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RESULT 8
AAH76218
ID AAH7
AC A
     16-FEB-2001; 2001WO-US05240
                                                                                                                                                                                                                                     PKIN; kinase; cytostatic; immunosuppressive; immunostimulant; antiarteriosclerotic; cardiant; gene therapy; antisense therap
                                         23-AUG-2001.
                                                                           #0200160991
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/product= "PKIN-10"
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Hafalia ;
Zingler ;
Nguyen Di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention provides human kinases (PKIN) and polynucleotides encoding PKIN. The PKIN polypeptides can be expressed using standard recombinant methodology. The PKIN polypeptides, polynucleotides, modulators and specific antibodies are useful in the diagnosis, treatment and prevention of cancer, immune disorders, disorders affecting growth and development, atherosclerosis, and other cardiovascular diseases, and lipid disorders and in the assessment of the effects of exogenous compounds on the expression of nucleic acid sequences of human kinases. The present sequence represents a cDNA encoding a human PKIN-10 polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          isolated human kinase polypeptides useful in the diagnosis, treatment and prevention of cancer, immune disorders and disorders affecting growth and development -
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KA, Lu DAM, Bandman O,
DB, Lal P, Walsh RT;
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Pred. No. 6.7e-133;
0; Mismatches 28;
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Burrill JD,
Griffin JA,
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                                            17-JUL-2001; 2001WO-IL00653.
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CC ABL39691 to ABL39818 represent novel human nucleic acid sequences CC (NS) can have cytostatic, osteopathic, gynaecological, neuroprotective, CC antirheumatic, antiarthritic, antipsoriatic, ophthalmological, virucide, CC vasotropic, antiarteriosclerotic, antiafertility, cardiovascular, cardiovascular, anti-HIV, antiinfertility, cardiovascular, cardiovascular, anticonvulsant, antidiabetic, tranquilliser, anticier, CC anticoagulant, anticonvulsant, antidiabetic, tranquilliser, antidicer, CC antidepressant, gastrointestinal, aeuroleptic, cerebroprotective, CC antidepressant, gastrointestinal, aeuroleptic, cerebroprotective, CC antidepressant, gastrointestinal, aeuroleptic, cerebroprotective, CC oncropic and contraceptive activities. The NS can be used in vaccines, CC gene thorapy and antisense therapy. Nucleic acids, expression vectors and CC diagnosing e.g. cancer, osteoporosis, endometriosis, degenerative CC disease, dystonia, multiple sclerosis, rheumatoid arthritis, psoriasis, CC glaucoma, obseity, muscular dystrophy, AIDS, infertility, cardiovascular CC disease, coagulation disease, ischaemia, hypertension, asthma, immune CC disease, epilepsy, angina, neurodegeneration, diabetes, anxiety, CC depression, schizophrenia, viral disease, gastric ulcers, stroke, CC Alzheimer's disease and as a contraceptive.
Query Match
Best Local Similarity
Matches 670; Conserva
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P-PSDB;
                                                                                        Sequence 1076 BP; 172 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     One hundred and twenty eight novel nucleic acid sequences, useful for treating and diagnosing e.g.\ cancer,\ asthma and Alzheimer's -
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15-DEC-2000; 2000IL-0140354.
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                  31.3%;
98.2%;
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Score 645.2; DB 24; Length 1076;
Pred. No. 4e-105;
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KW antirheumatic; antiarthritic; antipsortatic; ophthalmological; anti-HIV;
KW vasotropic; antiarteriosclerotic; antiinflammatory; dermatological;
KW anorectic; muscular; antiinfortility; cardiovascular; anticoagulant;
KW antifibrinolytic; hypotension; antiasthmatic; immunomodulator; cardiant;
KW anticonvulsant; antidiabetic; tranquilliser; antidepressnt; seuroleptic;
KW gastrointestinal; virucide; antiulcer; cerebroprotective; noctropic;
KW contraceptive; vaccine; gene therapy; cancer; osteoporosis; dystonia;
KW endometriosis; degenerative disease; multiple sclerosis; plaucoma;
KW rheumatoid arthritis; cataract; restenosis; atherosclerosis; glaucoma;
KW inflammation; skin disorder; obesity; muscular dystrophy; AIDS;
KW ischaemia; asthma; immune disease; congulation disease; hypertension;
KW ischaemia; asthma; immune disease; epilepsy; angina; neurodegeneration;
KW diabetes; anxiety; depression; schizophrenia; viral disease; stroke;
KW gastric ulcer; Alzheimer's disease; gene; ss.
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                              ABL39691 to ABL39818 represent novel human nucleic acid sequences encoding the proteins given in ABB6637 to ABB664. The novel sequences (NS) can have cytostatic, osteopathic, gymaecological, neuroprotective, antirheumatic, antiarthritic, antipporiatic, ophthalmological, virucide, vasotropic, antiarteriosclerotic, antiantiamatory, dermatological, vasotropic, antiarteriosclerotic, antiarterioscl
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RESULT 11 AAS91231/c ID AAS91231

AAS91231 standard; cDNA; 996 BP.

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                                                                                                                                                                                                                                                               The invention relates to isolated polynucleotide (I) and CC polypeptide (II) sequences. (I) is useful as hybridisation probes, CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome CC and gene mapping, and in recombinant production of (II). The CC and gene mapping, and in recombinant production of (II). The CC constraint promatal activity of (II) is useful in gene therapy techniques CC (II), (II) is useful for generating antibodies against it, detecting or CC (II), (II) is useful for generating antibodies against it, detecting or CC quantitating a polypeptide in tissue, as molecular weight markers and as CC as food supplement. (II) and its binding partners are useful in medical case of disorders involving aberrant protein expression or biological activity. CC diagnostics, forensics, gene mapping, identification of mutations in CC diagnostics, forensics, gene mapping, identification of mutations in CC diagnostics, forensics, gene mapping, identification of mutations (CC and to produce other types of data and products dependent on DNA and CC amino acid sequences. AAS64197-AAS94564 represent novel human CC diagnostic coding sequences of the invention.

CC The spolar coding sequences of the invention.

CC control the sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO CC at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                            Matches 860;
                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31-MAR-2000; 2000US-0540217.
23-AUG-2000; 2000US-0649167.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1, SEQ ID No 27035; 103pp; English.
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DB; ABG27044.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         n; chromosome mapping; gene mapping; gene therapy; forensic; supplement; medical imaging; diagnostic; genetic disorder; ss.
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                                                                                                                                        TGGACGAAGCCAGGGAAGAGGAGGGAGACAGAGAGAGTGGTTCTGTATGGCTAGGACCACC 1132
TGCCTCTGAACTGAGCCAAACCTTCAGTGCCTTCCAGAAGGGAGAAAGGCAGAAGCCTGT 1252
                                                                      CTACTACACGCTCAGCTGCCAACAGTGGATTGAGTTTTGGGGGGTAGCTCCAAGCCTTCTCC 119:
                                                                                                                                                                                                                                                             996 BP;
                                                   CTACTACACGCTCAGCTGCCAACAGTGGATTGAGTTTGGGGGGTAGCTCCAAGCCTTCTCC
                                                                                                                      TCGACGAAGCCAGGGAAGAGGGGAGACAGAGAAGTGGTTCTGTATGGCTAGGACCACC 917
                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                             248 A; 244 C; 251 G; 249 T; 4 other;
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Pred. No. 1.8e-90;
0; Mismatches 71; Indels 45;
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                                              Human; colon cancer; immunogenic; vaccine; tumour;
                                                                                                                      18-JUN-2002
                                                                               Human colon cancer-associated cDNA, SEQ ID No 580
                                                                                                                                                       ABK55110;
                                                                                                                                                                                         ABK55110 standard; cDNA; 541
                                                                                                                                                                                                                                                                                                               1988
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Best Local Similarity
Matches 536; Conserv
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02-OCT-2000;
20-MAR-2001;
03-JUL-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tumour polypeptides (II). (I) is useful for stimulating an immune response in a patient and treating colon cancer in a patient.
Oligonucleotides derived from (I) are useful for determining the presence of cancer in a patient. (I) and (II) are useful in pharmaceutical compositions, e.g. vaccines, and other compositions for the diagnosis and treatment of colon cancer. A composition comprising a first component selected from physiologically acceptable carriers and immunostimulants, and an antigen-presenting cell expressing (II) is useful for inhibiting development of cancer in a patient. (I) is useful in the design and preparation of ribozyme molecules for inhibiting expression of tumour polypeptides and (I). ABK5431-ABK55464 represent human colon cancer cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 315; 425pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel polynuclectide encoding colon tumour polypeptides, useful vaccines for treating colon cancers .
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                                                                       CATGACCATAGGTCACTGTCTACACTGGGTACACTTTGTACCAGTGTCGGCCTCCACTGA 1488
                                                                                                                                                                                                                                                                                                                                                         CACCCTACTACACGCTCAGCTGCCAACAGTGGATTGAGTTTGGGGGGTAGCTCCAAGCCTT 1188
                GACAATATTCCCTGCTCACAGAGATGACAAACTGGCATCCTTGAGCTGACAACACTTTTC
                                                                                                                                       GACAATATTCCCTGCTCACAGAGATGACAAACTGGCATCCTTGAGCTGACAACACTTTTC
                                                                                                                                                                 GGTGCTTATCAGGTGCCAAGCCCTGTTCTCGGTGCTGGGAGTACAGCAGTGAGCAAAGGA
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; 2000US-237406P.
; 2001US-277495P.
; 2001US-302702P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BP; 126 A; 146 C; 141 G; 128 T; 0 other;
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    isolated polynucleotides (I) encoding colon
    (I) is useful for stimulating an immune

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Pred. No. 2.6e-85;
D; Mismatches 5;
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RESULT 13
AAQ89817/c
ID AAQ89817;
XX
AC AAQ89817;
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C AAQ89817;
XX
C AAQ89817;
XX
C AAQ89817;
XX
DIT 25-MAR-2003 (updated)
DT 27-NOV-1995 (first entry)
XX
DNA encoding the AUF1 pol)
XX
AU-rich element RNA-bindir
XX
C-fos; cancer; ss.
XX
OS Homo sapiens.
XX
VOS Homo sapiens.
XX
VOS HOMO Sapiens.
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VOS511695-A1.
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VO9511695-A1.
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C1 O4-MAY-1995.
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DA (UYWA-) UNIV WAKE FOREST.
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PPD 04-MAY-1993; 93US-014642
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PPT 25-OCT-1993; 93US-014642
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C1 Seewer G;
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AUF1 polypeptide and DNA (PT POSDB; AAR74201.
XX
AUF1 polypeptide and DNA (PT POSDB; AAR74201.
XX
C1 The sequence is that of the CC of the AUF1 gene, so limit CC of the AUF1 gene, so limit CC cancer.
CC See also AAQ89818-20.
CC (Updated on 25-MAR-2003 to XX
XX
SQ Sequence 2562 BP; 663 A;
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                                                                                                                                                Query Match
Best Local S
Matches 566
                                                                                                                                                                                                                                                                                The sequence is that of the DNA encoding AUP1 (AU-rich element RNA-binding factor-1). AUP1 can be used to treat humans with low levels of the AUP1 gene, so limiting the expression of a proto-oncogene (pref. c-myc, c-myb or c-fos) which when over expressed, leads to
                                1577
                                                                                         1637
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                                                                                                                    604
                                                                                                                                                                Similarity
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GTGGGACCTGAGATACTCAGCTCACGGGCCTCATACTCGGGCAAGGCAGCCGATGTCTGG
                                                                                       TGACCCTTCTGTTTCTCCCCATGTCCCAGGAAGAAGCTGGTGCTGGAGAACCTGGAGGAC
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                                                  TCCTGCGTGCTGACTGGGCCAGATGATTCCCCTGTGGGACAAGCACGCGTGCCCAGCCTAC
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                                                                                                                                                                                                          BP; 663 A; 608 C; 788 G; 503 T; 0 other;
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                                                                                                                                                            Score 505.2; DB 16;
Pred. No. 2.7e-80;
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The present invention describes a composition (I) comprising: carries and immunostimulants, and a polypoptide (II) of a ovarian tumour polypoptide ended by a polynucleotide (III) having a cDNA sequence (81) from the 10912 nucleotide sequences as given in ABL77023 to ABL87934, (III) encoding (II) having a sequence (82), a T cell population of (II), or antigen presenting cells that express (II).
                                                                                                                                                                                                      Composition for therapy and diagnosis of ovarian cancer comprising polypeptide of a ovarian tumor polypeptide, polynucleotide encoding polypeptide, antibody specific to polypeptide or T cell expressing polypeptide -
                                                                                                                                                               Claim 1,
                                                                                                                                                                                                                                                                                                                           WPI; 2002-122075/16.
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                                                                                                                                                                                                                                                                                                                                                                        Jones
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Homo

sapiens

Human; Nove1 17-DEC-2001

cancer;

breast;

lung;

colon;

prostate;

cytostatic,

diagnostic;

human

(first

entry)

diagnostic and therapeutic gene

#519

13-SEP-2001 WO200166753-A2

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Best Local Similarity
Matches 426; Conserv
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Matches 335;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to new polynucleotides and polypeptides, useful for diagnosis and treatment of breast, lung and colon cancer. The sequences can be used in detecting differentially expressed genes correlated with a cancerous state of a mammalian cell, comprising detecting at least one differentially expressed gene product in a test sample derived from a cell suspected of being cancerous. They can also be used to inhibit tumour growth by modulating expression of a gene product. Ak336943-Ak33938 represent novel human diagnostic and therapeutic coding sequences of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Williams LT, Escobedo J, Innis MA, Garcia PD, Sudduth-Klir
Reinhard C, Randazzo F, Kennedy GC, Pot D, Kassam A, Lame
Drmanac R, Crkvenjakov R, Dickson M, Drmanac S, Labat I;
Leshkowitz D, Kita D, Garcia V, Jones WL, Stache-Crain B;
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Similarity 97.7%; Pred. No. 1.9e-49;
35; Conservative 0; Mismatches 8; Indels 0;
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               GCCCTGCACTGCCCTACAGGCACTGAGTATACCTGCAAGGTGT 343
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seam A, Lamson G;
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